

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Garoff, Henrik
Liljestrom, Peter
- (ii) TITLE OF INVENTION: DNA Expression Systems Based on
Alphaviruses
- (iii) NUMBER OF SEQUENCES: 27
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Birch, Stewart, Kolasch & Birch
(B) STREET: P.O. Box 747
(C) CITY: Falls Church
(D) STATE: Virginia
(E) COUNTRY: USA
(F) ZIP: 22040-0747
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 07/920,281
(B) FILING DATE: 13-AUG-1992
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Murphy Jr., Gerald M.
(B) REGISTRATION NUMBER: 28,977
(C) REFERENCE/DOCKET NUMBER: 828-103P
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 703-241-1300
(B) TELEFAX: 703-241-2848
(C) TELEX: 248345

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11517 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: RNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Semliki Forest Virus

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..11517

(D) OTHER INFORMATION: /label= genome
/note= "Semliki Forest Virus complete nucleotide
sequence, presented as a cloned DNA sequence; see
Figure 5."

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 87..7379

(D) OTHER INFORMATION: /product= "SFV polyprotein"

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 7421..11179

(D) OTHER INFORMATION: /product= "SFV polyprotein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GATGGCGGAT GTGTGACATA CACGACGCCA AAAGATTTTG TTCCAGCTCC TGCCACCTCC	60
GCTACGCGAG AGATTAACCA CCCACG ATG GCC GCC AAA GTG CAT GTT GAT ATT	113
Met Ala Ala Lys Val His Val Asp Ile	
1 5	
GAG GCT GAC AGC CCA TTC ATC AAG TCT TTG CAG AAG GCA TTT CCG TCG	161
Glu Ala Asp Ser Pro Phe Ile Lys Ser Leu Gln Lys Ala Phe Pro Ser	
10 15 20 25	
TTC GAG GTG GAG TCA TTG CAG GTC ACA CCA AAT GAC CAT GCA AAT GCC	209
Phe Glu Val Glu Ser Leu Gln Val Thr Pro Asn Asp His Ala Asn Ala	
30 35 40	
AGA GCA TTT TCG CAC CTG GCT ACC AAA TTG ATC GAG CAG GAG ACT GAC	257
Arg Ala Phe Ser His Leu Ala Thr Lys Leu Ile Glu Gln Glu Thr Asp	
45 50 55	
AAA GAC ACA CTC ATC TTG GAT ATC GGC AGT GCG CCT TCC AGG AGA ATG	305
Lys Asp Thr Leu Ile Leu Asp Ile Gly Ser Ala Pro Ser Arg Arg Met	
60 65 70	

ATG	TCT	ACG	CAC	AAA	TAC	CAC	TGC	GTA	TGC	CCT	ATG	CGC	AGC	GCA	GAA	353
Met	Ser	Thr	His	Lys	Tyr	His	Cys	Val	Cys	Pro	Met	Arg	Ser	Ala	Glu	
	75					80					85					
GAC	CCC	GAA	AGG	CTC	GAT	AGC	TAC	GCA	AAG	AAA	CTG	GCA	GCG	GCC	TCC	401
Asp	Pro	Glu	Arg	Leu	Asp	Ser	Tyr	Ala	Lys	Lys	Leu	Ala	Ala	Ala	Ser	
90					95					100					105	
GGG	AAG	GTG	CTG	GAT	AGA	GAG	ATC	GCA	GGA	AAA	ATC	ACC	GAC	CTG	CAG	449
Gly	Lys	Val	Leu	Asp	Arg	Glu	Ile	Ala	Gly	Lys	Ile	Thr	Asp	Leu	Gln	
				110					115					120		
ACC	GTC	ATG	GCT	ACG	CCA	GAC	GCT	GAA	TCT	CCT	ACC	TTT	TGC	CTG	CAT	497
Thr	Val	Met	Ala	Thr	Pro	Asp	Ala	Glu	Ser	Pro	Thr	Phe	Cys	Leu	His	
			125					130					135			
ACA	GAC	GTC	ACG	TGT	CGT	ACG	GCA	GCC	GAA	GTG	GCC	GTA	TAC	CAG	GAC	545
Thr	Asp	Val	Thr	Cys	Arg	Thr	Ala	Ala	Glu	Val	Ala	Val	Tyr	Gln	Asp	
	140						145					150				
GTG	TAT	GCT	GTA	CAT	GCA	CCA	ACA	TCG	CTG	TAC	CAT	CAG	GCG	ATG	AAA	593
Val	Tyr	Ala	Val	His	Ala	Pro	Thr	Ser	Leu	Tyr	His	Gln	Ala	Met	Lys	
	155					160					165					
GGT	GTC	AGA	ACG	GCG	TAT	TGG	ATT	GGG	TTT	GAC	ACC	ACC	CCG	TTT	ATG	641
Gly	Val	Arg	Thr	Ala	Tyr	Trp	Ile	Gly	Phe	Asp	Thr	Thr	Pro	Phe	Met	
170					175					180					185	
TTT	GAC	GCG	CTA	GCA	GGC	GCG	TAT	CCA	ACC	TAC	GCC	ACA	AAC	TGG	GCC	689
Phe	Asp	Ala	Leu	Ala	Gly	Ala	Tyr	Pro	Thr	Tyr	Ala	Thr	Asn	Trp	Ala	
				190					195					200		
TGAC	GAG	CAG	GTG	TTA	CAG	GCC	AGG	AAC	ATA	GGA	CTG	TGT	GCA	GCA	TCC	737
Asp	Glu	Gln	Val	Leu	Gln	Ala	Arg	Asn	Ile	Gly	Leu	Cys	Ala	Ala	Ser	
			205					210					215			
TTG	ACT	GAG	GGA	AGA	CTC	GGC	AAA	CTG	TCC	ATT	CTC	CGC	AAG	AAG	CAA	785
Leu	Thr	Glu	Gly	Arg	Leu	Gly	Lys	Leu	Ser	Ile	Leu	Arg	Lys	Lys	Gln	
		220					225					230				
TTG	AAA	CCT	TGC	GAC	ACA	GTC	ATG	TTC	TCG	GTA	GGA	TCT	ACA	TTG	TAC	833
Leu	Lys	Pro	Cys	Asp	Thr	Val	Met	Phe	Ser	Val	Gly	Ser	Thr	Leu	Tyr	
	235					240					245					
ACT	GAG	AGC	AGA	AAG	CTA	CTG	AGG	AGC	TGG	CAC	TTA	CCC	TCC	GTA	TTC	881
Thr	Glu	Ser	Arg	Lys	Leu	Leu	Arg	Ser	Trp	His	Leu	Pro	Ser	Val	Phe	
250					255					260					265	
CAC	CTG	AAA	GGT	AAA	CAA	TCC	TTT	ACC	TGT	AGG	TGC	GAT	ACC	ATC	GTA	929
His	Leu	Lys	Gly	Lys	Gln	Ser	Phe	Thr	Cys	Arg	Cys	Asp	Thr	Ile	Val	
				270					275					280		

TCA	TGT	GAA	GGG	TAC	GTA	GTT	AAG	AAA	ATC	ACT	ATG	TGC	CCC	GGC	CTG	977
Ser	Cys	Glu	Gly	Tyr	Val	Val	Lys	Lys	Ile	Thr	Met	Cys	Pro	Gly	Leu	
			285					290					295			
TAC	GGT	AAA	ACG	GTA	GGG	TAC	GCC	GTG	ACG	TAT	CAC	GCG	GAG	GGA	TTC	1025
Tyr	Gly	Lys	Thr	Val	Gly	Tyr	Ala	Val	Thr	Tyr	His	Ala	Glu	Gly	Phe	
		300					305					310				
CTA	GTG	TGC	AAG	ACC	ACA	GAC	ACT	GTC	AAA	GGA	GAA	AGA	GTC	TCA	TTC	1073
Leu	Val	Cys	Lys	Thr	Thr	Asp	Thr	Val	Lys	Gly	Glu	Arg	Val	Ser	Phe	
	315					320					325					
CCT	GTA	TGC	ACC	TAC	GTC	CCC	TCA	ACC	ATC	TGT	GAT	CAA	ATG	ACT	GGC	1121
Pro	Val	Cys	Thr	Tyr	Val	Pro	Ser	Thr	Ile	Cys	Asp	Gln	Met	Thr	Gly	
330					335					340					345	
ATA	CTA	GCG	ACC	GAC	GTC	ACA	CCG	GAG	GAC	GCA	CAG	AAG	TTG	TTA	GTG	1169
Ile	Leu	Ala	Thr	Asp	Val	Thr	Pro	Glu	Asp	Ala	Gln	Lys	Leu	Leu	Val	
				350					355					360		
GGA	TTG	AAT	CAG	AGG	ATA	GTT	GTG	AAC	GGA	AGA	ACA	CAG	CGA	AAC	ACT	1217
Gly	Leu	Asn	Gln	Arg	Ile	Val	Val	Asn	Gly	Arg	Thr	Gln	Arg	Asn	Thr	
			365					370					375			
AAC	ACG	ATG	AAG	AAC	TAT	CTG	CTT	CCG	ATT	GTG	GCC	GTC	GCA	TTT	AGC	1265
Asn	Thr	Met	Lys	Asn	Tyr	Leu	Leu	Pro	Ile	Val	Ala	Val	Ala	Phe	Ser	
		380					385					390				
AAG	TGG	GCG	AGG	GAA	TAC	AAG	GCA	GAC	CTT	GAT	GAT	GAA	AAA	CCT	CTG	1313
Lys	Trp	Ala	Arg	Glu	Tyr	Lys	Ala	Asp	Leu	Asp	Asp	Glu	Lys	Pro	Leu	
	395					400					405					
GGT	GTC	CGA	GAG	AGG	TCA	CTT	ACT	TGC	TGC	TGC	TTG	TGG	GCA	TTT	AAA	1361
Gly	Val	Arg	Glu	Arg	Ser	Leu	Thr	Cys	Cys	Cys	Leu	Trp	Ala	Phe	Lys	
410					415					420					425	
ACG	AGG	AAG	ATG	CAC	ACC	ATG	TAC	AAG	AAA	CCA	GAC	ACC	CAG	ACA	ATA	1409
Thr	Arg	Lys	Met	His	Thr	Met	Tyr	Lys	Lys	Pro	Asp	Thr	Gln	Thr	Ile	
				430					435					440		
GTG	AAG	GTG	CCT	TCA	GAG	TTT	AAC	TCG	TTC	GTC	ATC	CCG	AGC	CTA	TGG	1457
Val	Lys	Val	Pro	Ser	Glu	Phe	Asn	Ser	Phe	Val	Ile	Pro	Ser	Leu	Trp	
			445					450					455			
TCT	ACA	GGC	CTC	GCA	ATC	CCA	GTC	AGA	TCA	CGC	ATT	AAG	ATG	CTT	TTG	1505
Ser	Thr	Gly	Leu	Ala	Ile	Pro	Val	Arg	Ser	Arg	Ile	Lys	Met	Leu	Leu	
		460					465					470				
GCC	AAG	AAG	ACC	AAG	CGA	GAG	TTA	ATA	CCT	GTT	CTC	GAC	GCG	TCG	TCA	1553
Ala	Lys	Lys	Thr	Lys	Arg	Glu	Leu	Ile	Pro	Val	Leu	Asp	Ala	Ser	Ser	
	475					480					485					

GCC Ala 490	AGG Arg	GAT Asp	GCT Ala	GAA Glu	CAA Gln 495	GAG Glu	GAG Glu	AAG Lys	GAG Glu	AGG Arg 500	TTG Leu	GAG Glu	GCC Ala	GAG Glu	CTG Leu 505	1601
ACT Thr	AGA Arg	GAA Glu	GCC Ala	TTA Leu 510	CCA Pro	CCC Pro	CTC Leu	GTC Val	CCC Pro 515	ATC Ile	GCG Ala	CCG Pro	GCG Ala	GAG Glu 520	ACG Thr	1649
GGA Gly	GTC Val	GTC Val	GAC Asp 525	GTC Val	GAC Asp	GTT Val	GAA Glu	GAA Glu 530	CTA Leu	GAG Glu	TAT Tyr	CAC His	GCA Ala 535	GGT Gly	GCA Ala	1697
GGG Gly	GTC Val	GTG Val 540	GAA Glu	ACA Thr	CCT Pro	CGC Arg	AGC Ser 545	GCG Ala	TTG Leu	AAA Lys	GTC Val	ACC Thr 550	GCA Ala	CAG Gln	CCG Pro	1745
AAC Asn 555	GAC Asp	GTA Val	CTA Leu	CTA Leu	GGA Gly	AAT Asn 560	TAC Tyr	GTA Val	GTT Val	CTG Leu	TCC Ser 565	CCG Pro	CAG Gln	ACC Thr	GTG Val	1793
CTC Leu 570	AAG Lys	AGC Ser	TCC Ser	AAG Lys	TTG Leu 575	GCC Ala	CCC Pro	GTG Val	CAC His	CCT Pro 580	CTA Leu	GCA Ala	GAG Glu	CAG Gln	GTG Val 585	1841
AAA Lys	ATA Ile	ATA Ile	ACA Thr	CAT His 590	AAC Asn	GGG Gly	AGG Arg	GCC Ala	GGC Gly 595	GGT Gly	TAC Tyr	CAG Gln	GTC Val	GAC Asp 600	GGA Gly	1889
TAT Tyr	GAC Asp	GGC Gly	AGG Arg 605	GTC Val	CTA Leu	CTA Leu	CCA Pro	TGT Cys 610	GGA Gly	TCG Ser	GCC Ala	ATT Ile	CCG Pro 615	GTC Val	CCT Pro	1937
GAG Glu	TTT Phe	CAA Gln 620	GCT Ala	TTG Leu	AGC Ser	GAG Glu	AGC Ser 625	GCC Ala	ACT Thr	ATG Met	GTG Val	TAC Tyr 630	AAC Asn	GAA Glu	AGG Arg	1985
GAG Glu 635	TTC Phe	GTC Val	AAC Asn	AGG Arg	AAA Lys	CTA Leu 640	TAC Tyr	CAT His	ATT Ile	GCC Ala	GTT Val 645	CAC His	GGA Gly	CCG Pro	TCG Ser	2033
CTG Leu 650	AAC Asn	ACC Thr	GAC Asp	GAG Glu	GAG Glu 655	AAC Asn	TAC Tyr	GAG Glu	AAA Lys	GTC Val 660	AGA Arg	GCT Ala	GAA Glu	AGA Arg	ACT Thr 665	2081
GAC Asp	GCC Ala	GAG Glu	TAC Tyr	GTG Val 670	TTC Phe	GAC Asp	GTA Val	GAT Asp	AAA Lys 675	AAA Lys	TGC Cys	TGC Cys	GTC Val	AAG Lys 680	AGA Arg	2129
GAG Glu	GAA Glu	GCG Ala	TCG Ser 685	GGT Gly	TTG Leu	GTG Val	TTG Leu	GTG Val 690	GGA Gly	GAG Glu	CTA Leu	ACC Thr	AAC Asn 695	CCC Pro	CCG Pro	2177

TTC	CAT	GAA	TTC	GCC	TAC	GAA	GGG	CTG	AAG	ATC	AGG	CCG	TCG	GCA	CCA	2225
Phe	His	Glu	Phe	Ala	Tyr	Glu	Gly	Leu	Lys	Ile	Arg	Pro	Ser	Ala	Pro	
		700					705					710				
TAT	AAG	ACT	ACA	GTA	GTA	GGA	GTC	TTT	GGG	GTT	CCG	GGA	TCA	GGC	AAG	2273
Tyr	Lys	Thr	Thr	Val	Val	Gly	Val	Phe	Gly	Val	Pro	Gly	Ser	Gly	Lys	
	715					720					725					
TCT	GCT	ATT	ATT	AAG	AGC	CTC	GTG	ACC	AAA	CAC	GAT	CTG	GTC	ACC	AGC	2321
Ser	Ala	Ile	Ile	Lys	Ser	Leu	Val	Thr	Lys	His	Asp	Leu	Val	Thr	Ser	
	730				735					740					745	
GGC	AAG	AAG	GAG	AAC	TGC	CAG	GAA	ATA	GTT	AAC	GAC	GTG	AAG	AAG	CAC	2369
Gly	Lys	Lys	Glu	Asn	Cys	Gln	Glu	Ile	Val	Asn	Asp	Val	Lys	Lys	His	
				750					755						760	
CGC	GGG	AAG	GGG	ACA	AGT	AGG	GAA	AAC	AGT	GAC	TCC	ATC	CTG	CTA	AAC	2417
Arg	Gly	Lys	Gly	Thr	Ser	Arg	Glu	Asn	Ser	Asp	Ser	Ile	Leu	Leu	Asn	
			765					770					775			
GGG	TGT	CGT	CGT	GCC	GTG	GAC	ATC	CTA	TAT	GTG	GAC	GAG	GCT	TTC	GCT	2465
Gly	Cys	Arg	Arg	Ala	Val	Asp	Ile	Leu	Tyr	Val	Asp	Glu	Ala	Phe	Ala	
		780					785					790				
TGC	CAT	TCC	GGT	ACT	CTG	CTG	GCC	CTA	ATT	GCT	CTT	GTT	AAA	CCT	CGG	2513
Cys	His	Ser	Gly	Thr	Leu	Leu	Ala	Leu	Ile	Ala	Leu	Val	Lys	Pro	Arg	
	795					800					805					
AGC	AAA	GTG	GTG	TTA	TGC	GGA	GAC	CCC	AAG	CAA	TGC	GGA	TTC	TTC	AAT	2561
Ser	Lys	Val	Val	Leu	Cys	Gly	Asp	Pro	Lys	Gln	Cys	Gly	Phe	Phe	Asn	
	810				815					820					825	
ATG	ATG	CAG	CTT	AAG	GTG	AAC	TTC	AAC	CAC	AAC	ATC	TGC	ACT	GAA	GTA	2609
Met	Met	Gln	Leu	Lys	Val	Asn	Phe	Asn	His	Asn	Ile	Cys	Thr	Glu	Val	
				830					835					840		
TGT	CAT	AAA	AGT	ATA	TCC	AGA	CGT	TGC	ACG	CGT	CCA	GTC	ACG	GCC	ATC	2657
Cys	His	Lys	Ser	Ile	Ser	Arg	Arg	Cys	Thr	Arg	Pro	Val	Thr	Ala	Ile	
			845					850					855			
GTG	TCT	ACG	TTG	CAC	TAC	GGA	GGC	AAG	ATG	CGC	ACG	ACC	AAC	CCG	TGC	2705
Val	Ser	Thr	Leu	His	Tyr	Gly	Gly	Lys	Met	Arg	Thr	Thr	Asn	Pro	Cys	
		860					865					870				
AAC	AAA	CCC	ATA	ATC	ATA	GAC	ACC	ACA	GGA	CAG	ACC	AAG	CCC	AAG	CCA	2753
Asn	Lys	Pro	Ile	Ile	Ile	Asp	Thr	Thr	Gly	Gln	Thr	Lys	Pro	Lys	Pro	
	875					880					885					
GGA	GAC	ATC	GTG	TTA	ACA	TGC	TTC	CGA	GGC	TGG	GCA	AAG	CAG	CTG	CAG	2801
Gly	Asp	Ile	Val	Leu	Thr	Cys	Phe	Arg	Gly	Trp	Ala	Lys	Gln	Leu	Gln	
	890				895					900					905	

TTG	GAC	TAC	CGT	GGA	CAC	GAA	GTC	ATG	ACA	GCA	GCA	GCA	TCT	CAG	GGC	2849
Leu	Asp	Tyr	Arg	Gly	His	Glu	Val	Met	Thr	Ala	Ala	Ala	Ser	Gln	Gly	
				910					915					920		
CTC	ACC	CGC	AAA	GGG	GTA	TAC	GCC	GTA	AGG	CAG	AAG	GTG	AAT	GAA	AAT	2897
Leu	Thr	Arg	Lys	Gly	Val	Tyr	Ala	Val	Arg	Gln	Lys	Val	Asn	Glu	Asn	
			925					930					935			
CCC	TTG	TAT	GCC	CCT	GCG	TCG	GAG	CAC	GTG	AAT	GTA	CTG	CTG	ACG	CGC	2945
Pro	Leu	Tyr	Ala	Pro	Ala	Ser	Glu	His	Val	Asn	Val	Leu	Leu	Thr	Arg	
		940					945					950				
ACT	GAG	GAT	AGG	CTG	GTG	TGG	AAA	ACG	CTG	GCC	GGC	GAT	CCC	TGG	ATT	2993
Thr	Glu	Asp	Arg	Leu	Val	Trp	Lys	Thr	Leu	Ala	Gly	Asp	Pro	Trp	Ile	
	955					960					965					
AAG	GTC	CTA	TCA	AAC	ATT	CCA	CAG	GGT	AAC	TTT	ACG	GCC	ACA	TTG	GAA	3041
Lys	Val	Leu	Ser	Asn	Ile	Pro	Gln	Gly	Asn	Phe	Thr	Ala	Thr	Leu	Glu	
970					975					980					985	
GAA	TGG	CAA	GAA	GAA	CAC	GAC	AAA	ATA	ATG	AAG	GTG	ATT	GAA	GGA	CCG	3089
Glu	Trp	Gln	Glu	Glu	His	Asp	Lys	Ile	Met	Lys	Val	Ile	Glu	Gly	Pro	
				990					995					1000		
GCT	GCG	CCT	GTG	GAC	GCG	TTC	CAG	AAC	AAA	GCG	AAC	GTG	TGT	TGG	GCG	3137
Ala	Ala	Pro	Val	Asp	Ala	Phe	Gln	Asn	Lys	Ala	Asn	Val	Cys	Trp	Ala	
			1005					1010					1015			
AAA	AGC	CTG	GTG	CCT	GTC	CTG	GAC	ACT	GCC	GGA	ATC	AGA	TTG	ACA	GCA	3185
Lys	Ser	Leu	Val	Pro	Val	Leu	Asp	Thr	Ala	Gly	Ile	Arg	Leu	Thr	Ala	
		1020					1025					1030				
GAG	GAG	TGG	AGC	ACC	ATA	ATT	ACA	GCA	TTT	AAG	GAG	GAC	AGA	GCT	TAC	3233
Glu	Glu	Trp	Ser	Thr	Ile	Ile	Thr	Ala	Phe	Lys	Glu	Asp	Arg	Ala	Tyr	
	1035					1040					1045					
TCT	CCA	GTG	GTG	GCC	TTG	AAT	GAA	ATT	TGC	ACC	AAG	TAC	TAT	GGA	GTT	3281
Ser	Pro	Val	Val	Ala	Leu	Asn	Glu	Ile	Cys	Thr	Lys	Tyr	Tyr	Gly	Val	
	1050				1055					1060					1065	
GAC	CTG	GAC	AGT	GGC	CTG	TTT	TCT	GCC	CCG	AAG	GTG	TCC	CTG	TAT	TAC	3329
Asp	Leu	Asp	Ser	Gly	Leu	Phe	Ser	Ala	Pro	Lys	Val	Ser	Leu	Tyr	Tyr	
				1070					1075					1080		
GAG	AAC	AAC	CAC	TGG	GAT	AAC	AGA	CCT	GGT	GGA	AGG	ATG	TAT	GGA	TTC	3377
Glu	Asn	Asn	His	Trp	Asp	Asn	Arg	Pro	Gly	Gly	Arg	Met	Tyr	Gly	Phe	
			1085					1090					1095			
AAT	GCC	GCA	ACA	GCT	GCC	AGG	CTG	GAA	GCT	AGA	CAT	ACC	TTC	CTG	AAG	3425
Asn	Ala	Ala	Thr	Ala	Ala	Arg	Leu	Glu	Ala	Arg	His	Thr	Phe	Leu	Lys	
		1100					1105					1110				

GGG CAG TGG CAT ACG GGC AAG CAG GCA GTT ATC GCA GAA AGA AAA ATC Gly Gln Trp His Thr Gly Lys Gln Ala Val Ile Ala Glu Arg Lys Ile 1115 1120 1125	3473
CAA CCG CTT TCT GTG CTG GAC AAT GTA ATT CCT ATC AAC CGC AGG CTG Gln Pro Leu Ser Val Leu Asp Asn Val Ile Pro Ile Asn Arg Arg Leu 1130 1135 1140 1145	3521
CCG CAC GCC CTG GTG GCT GAG TAC AAG ACG GTT AAA GGC AGT AGG GTT Pro His Ala Leu Val Ala Glu Tyr Lys Thr Val Lys Gly Ser Arg Val 1150 1155 1160	3569
GAG TGG CTG GTC AAT AAA GTA AGA GGG TAC CAC GTC CTG CTG GTG AGT Glu Trp Leu Val Asn Lys Val Arg Gly Tyr His Val Leu Leu Val Ser 1165 1170 1175	3617
GAG TAC AAC CTG GCT TTG CCT CGA CGC AGG GTC ACT TGG TTG TCA CCG Glu Tyr Asn Leu Ala Leu Pro Arg Arg Arg Val Thr Trp Leu Ser Pro 1180 1185 1190	3665
CTG AAT GTC ACA GGC GCC GAT AGG TGC TAC GAC CTA AGT TTA GGA CTG Leu Asn Val Thr Gly Ala Asp Arg Cys Tyr Asp Leu Ser Leu Gly Leu 1195 1200 1205	3713
CCG GCT GAC GCC GGC AGG TTC GAC TTG GTC TTT GTG AAC ATT CAC ACG Pro Ala Asp Ala Gly Arg Phe Asp Leu Val Phe Val Asn Ile His Thr 1210 1215 1220 1225	3761
GAA TTC AGA ATC CAC CAC TAC CAG CAG TGT GTC GAC CAC GCC ATG AAG Glu Phe Arg Ile His His Tyr Gln Gln Cys Val Asp His Ala Met Lys 1230 1235 1240	3809
CTG CAG ATG CTT GGG GGA GAT GCG CTA CGA CTG CTA AAA CCC GGC GGC Leu Gln Met Leu Gly Gly Asp Ala Leu Arg Leu Leu Lys Pro Gly Gly 1245 1250 1255	3857
ATC TTG ATG AGA GCT TAC GGA TAC GCC GAT AAA ATC AGC GAA GCC GTT Ile Leu Met Arg Ala Tyr Gly Tyr Ala Asp Lys Ile Ser Glu Ala Val 1260 1265 1270	3905
GTT TCC TCC TTA AGC AGA AAG TTC TCG TCT GCA AGA GTG TTG CGC CCG Val Ser Ser Leu Ser Arg Lys Phe Ser Ser Ala Arg Val Leu Arg Pro 1275 1280 1285	3953
GAT TGT GTC ACC AGC AAT ACA GAA GTG TTC TTG CTG TTC TCC AAC TTT Asp Cys Val Thr Ser Asn Thr Glu Val Phe Leu Leu Phe Ser Asn Phe 1290 1295 1300 1305	4001
GAC AAC GGA AAG AGA CCC TCT ACG CTA CAC CAG ATG AAT ACC AAG CTG Asp Asn Gly Lys Arg Pro Ser Thr Leu His Gln Met Asn Thr Lys Leu 1310 1315 1320	4049

GGG TCG CTG TAC TCG TAC TTT GAA GGT ACG AAA TTC AAC CAG GCT GCT	4721
Gly Ser Leu Tyr Ser Tyr Phe Glu Gly Thr Lys Phe Asn Gln Ala Ala	
1530 1535 1540 1545	
ATT GAT ATG GCA GAG ATA CTG ACG TTG TGG CCC AGA CTG CAA GAG GCA	4769
Ile Asp Met Ala Glu Ile Leu Thr Leu Trp Pro Arg Leu Gln Glu Ala	
1550 1555 1560	
AAC GAA CAG ATA TGC CTA TAC GCG CTG GGC GAA ACA ATG GAC AAC ATC	4817
Asn Glu Gln Ile Cys Leu Tyr Ala Leu Gly Glu Thr Met Asp Asn Ile	
1565 1570 1575	
AGA TCC AAA TGT CCG GTG AAC GAT TCC GAT TCA TCA ACA CCT CCC AGG	4865
Arg Ser Lys Cys Pro Val Asn Asp Ser Asp Ser Ser Thr Pro Pro Arg	
1580 1585 1590	
ACA GTG CCC TGC CTG TGC CGC TAC GCA ATG ACA GCA GAA CGG ATC GCC	4913
Thr Val Pro Cys Leu Cys Arg Tyr Ala Met Thr Ala Glu Arg Ile Ala	
1595 1600 1605	
CGC CTT AGG TCA CAC CAA GTT AAA AGC ATG GTG GTT TGC TCA TCT TTT	4961
Arg Leu Arg Ser His Gln Val Lys Ser Met Val Val Cys Ser Ser Phe	
1610 1615 1620 1625	
CCC CTC CCG AAA TAC CAT GTA GAT GGG GTG CAG AAG GTA AAG TGC GAG	5009
Pro Leu Pro Lys Tyr His Val Asp Gly Val Gln Lys Val Lys Cys Glu	
1630 1635 1640	
AAG GTT CTC CTG TTC GAC CCG ACG GTA CCT TCA GTG GTT AGT CCG CGG	5057
Lys Val Leu Leu Phe Asp Pro Thr Val Pro Ser Val Val Ser Pro Arg	
1645 1650 1655	
AAG TAT GCC GCA TCT ACG ACG GAC CAC TCA GAT CGG TCG TTA CGA GGG	5105
Lys Tyr Ala Ala Ser Thr Thr Asp His Ser Asp Arg Ser Leu Arg Gly	
1660 1665 1670	
TTT GAC TTG GAC TGG ACC ACC GAC TCG TCT TCC ACT GCC AGC GAT ACC	5153
Phe Asp Leu Asp Trp Thr Thr Asp Ser Ser Ser Thr Ala Ser Asp Thr	
1675 1680 1685	
ATG TCG CTA CCC AGT TTG CAG TCG TGT GAC ATC GAC TCG ATC TAC GAG	5201
Met Ser Leu Pro Ser Leu Gln Ser Cys Asp Ile Asp Ser Ile Tyr Glu	
1690 1695 1700 1705	
CCA ATG GCT CCC ATA GTA GTG ACG GCT GAC GTA CAC CCT GAA CCC GCA	5249
Pro Met Ala Pro Ile Val Val Thr Ala Asp Val His Pro Glu Pro Ala	
1710 1715 1720	
GGC ATC GCG GAC CTG GCG GCA GAT GTG CAC CCT GAA CCC GCA GAC CAT	5297
Gly Ile Ala Asp Leu Ala Ala Asp Val His Pro Glu Pro Ala Asp His	
1725 1730 1735	

GTG	GAC	CTC	GAG	AAC	CCG	ATT	CCT	CCA	CCG	CGC	CCG	AAG	AGA	GCT	GCA	5345
Val	Asp	Leu	Glu	Asn	Pro	Ile	Pro	Pro	Pro	Arg	Pro	Lys	Arg	Ala	Ala	
		1740					1745					1750				
TAC	CTT	GCC	TCC	CGC	GCG	GCG	GAG	CGA	CCG	GTG	CCG	GCG	CCG	AGA	AAG	5393
Tyr	Leu	Ala	Ser	Arg	Ala	Ala	Glu	Arg	Pro	Val	Pro	Ala	Pro	Arg	Lys	
	1755					1760					1765					
CCG	ACG	CCT	GCC	CCA	AGG	ACT	GCG	TTT	AGG	AAC	AAG	CTG	CCT	TTG	ACG	5441
Pro	Thr	Pro	Ala	Pro	Arg	Thr	Ala	Phe	Arg	Asn	Lys	Leu	Pro	Leu	Thr	
1770					1775					1780					1785	
TTC	GGC	GAC	TTT	GAC	GAG	CAC	GAG	GTC	GAT	GCG	TTG	GCC	TCC	GGG	ATT	5489
Phe	Gly	Asp	Phe	Asp	Glu	His	Glu	Val	Asp	Ala	Leu	Ala	Ser	Gly	Ile	
			1790						1795					1800		
ACT	TTC	GGA	GAC	TTC	GAC	GAC	GTC	CTG	CGA	CTA	GGC	CGC	GCG	GGT	GCA	5537
Thr	Phe	Gly	Asp	Phe	Asp	Asp	Val	Leu	Arg	Leu	Gly	Arg	Ala	Gly	Ala	
			1805					1810					1815			
TAT	ATT	TTC	TCC	TCG	GAC	ACT	GGC	AGC	GGA	CAT	TTA	CAA	CAA	AAA	TCC	5585
Tyr	Ile	Phe	Ser	Ser	Asp	Thr	Gly	Ser	Gly	His	Leu	Gln	Gln	Lys	Ser	
	1820						1825					1830				
GTT	AGG	CAG	CAC	AAT	CTC	CAG	TGC	GCA	CAA	CTG	GAT	GCG	GTC	CAG	GAG	5633
Val	Arg	Gln	His	Asn	Leu	Gln	Cys	Ala	Gln	Leu	Asp	Ala	Val	Gln	Glu	
	1835					1840					1845					
GAG	AAA	ATG	TAC	CCG	CCA	AAA	TTG	GAT	ACT	GAG	AGG	GAG	AAG	CTG	TTG	5681
Glu	Lys	Met	Tyr	Pro	Pro	Lys	Leu	Asp	Thr	Glu	Arg	Glu	Lys	Leu	Leu	
1850					1855					1860					1865	
CTG	CTG	AAA	ATG	CAG	ATG	CAC	CCA	TCG	GAG	GCT	AAT	AAG	AGT	CGA	TAC	5729
Leu	Leu	Lys	Met	Gln	Met	His	Pro	Ser	Glu	Ala	Asn	Lys	Ser	Arg	Tyr	
				1870					1875					1880		
CAG	TCT	CGC	AAA	GTG	GAG	AAC	ATG	AAA	GCC	ACG	GTG	GTG	GAC	AGG	CTC	5777
Gln	Ser	Arg	Lys	Val	Glu	Asn	Met	Lys	Ala	Thr	Val	Val	Asp	Arg	Leu	
			1885					1890					1895			
ACA	TCG	GGG	GCC	AGA	TTG	TAC	ACG	GGA	GCG	GAC	GTA	GGC	CGC	ATA	CCA	5825
Thr	Ser	Gly	Ala	Arg	Leu	Tyr	Thr	Gly	Ala	Asp	Val	Gly	Arg	Ile	Pro	
	1900						1905					1910				
ACA	TAC	GCG	GTT	CGG	TAC	CCC	CGC	CCC	GTG	TAC	TCC	CCT	ACC	GTG	ATC	5873
Thr	Tyr	Ala	Val	Arg	Tyr	Pro	Arg	Pro	Val	Tyr	Ser	Pro	Thr	Val	Ile	
	1915					1920					1925					
GAA	AGA	TTC	TCA	AGC	CCC	GAT	GTA	GCA	ATC	GCA	GCG	TGC	AAC	GAA	TAC	5921
Glu	Arg	Phe	Ser	Ser	Pro	Asp	Val	Ala	Ile	Ala	Ala	Cys	Asn	Glu	Tyr	
1930					1935					1940					1945	

CTA	TCC	AGA	AAT	TAC	CCA	ACA	GTG	GCG	TCG	TAC	CAG	ATA	ACA	GAT	GAA	5969
Leu	Ser	Arg	Asn	Tyr	Pro	Thr	Val	Ala	Ser	Tyr	Gln	Ile	Thr	Asp	Glu	
				1950					1955					1960		
TAC	GAC	GCA	TAC	TTG	GAC	ATG	GTT	GAC	GGG	TCG	GAT	AGT	TGC	TTG	GAC	6017
Tyr	Asp	Ala	Tyr	Leu	Asp	Met	Val	Asp	Gly	Ser	Asp	Ser	Cys	Leu	Asp	
			1965					1970					1975			
AGA	GCG	ACA	TTC	TGC	CCG	GCG	AAG	CTC	CGG	TGC	TAC	CCG	AAA	CAT	CAT	6065
Arg	Ala	Thr	Phe	Cys	Pro	Ala	Lys	Leu	Arg	Cys	Tyr	Pro	Lys	His	His	
		1980					1985					1990				
GCG	TAC	CAC	CAG	CCG	ACT	GTA	CGC	AGT	GCC	GTC	CCG	TCA	CCC	TTT	CAG	6113
Ala	Tyr	His	Gln	Pro	Thr	Val	Arg	Ser	Ala	Val	Pro	Ser	Pro	Phe	Gln	
	1995					2000					2005					
AAC	ACA	CTA	CAG	AAC	GTG	CTA	GCG	GCC	GCC	ACC	AAG	AGA	AAC	TGC	AAC	6161
Asn	Thr	Leu	Gln	Asn	Val	Leu	Ala	Ala	Ala	Thr	Lys	Arg	Asn	Cys	Asn	
2010					2015					2020					2025	
GTC	ACG	CAA	ATG	CGA	GAA	CTA	CCC	ACC	ATG	GAC	TCG	GCA	GTG	TTC	AAC	6209
Val	Thr	Gln	Met	Arg	Glu	Leu	Pro	Thr	Met	Asp	Ser	Ala	Val	Phe	Asn	
				2030					2035					2040		
GTG	GAG	TGC	TTC	AAG	CGC	TAT	GCC	TGC	TCC	GGA	GAA	TAT	TGG	GAA	GAA	6257
Val	Glu	Cys	Phe	Lys	Arg	Tyr	Ala	Cys	Ser	Gly	Glu	Tyr	Trp	Glu	Glu	
			2045					2050					2055			
TAT	GCT	AAA	CAA	CCT	ATC	CGG	ATA	ACC	ACT	GAG	AAC	ATC	ACT	ACC	TAT	6305
Tyr	Ala	Lys	Gln	Pro	Ile	Arg	Ile	Thr	Thr	Glu	Asn	Ile	Thr	Thr	Tyr	
		2060					2065					2070				
GTG	ACC	AAA	TTG	AAA	GGC	CCG	AAA	GCT	GCT	GCC	TTG	TTC	GCT	AAG	ACC	6353
Val	Thr	Lys	Leu	Lys	Gly	Pro	Lys	Ala	Ala	Ala	Leu	Phe	Ala	Lys	Thr	
	2075					2080					2085					
CAC	AAC	TTG	GTT	CCG	CTG	CAG	GAG	GTT	CCC	ATG	GAC	AGA	TTC	ACG	GTC	6401
His	Asn	Leu	Val	Pro	Leu	Gln	Glu	Val	Pro	Met	Asp	Arg	Phe	Thr	Val	
2090					2095					2100					2105	
GAC	ATG	AAA	CGA	GAT	GTC	AAA	GTC	ACT	CCA	GGG	ACG	AAA	CAC	ACA	GAG	6449
Asp	Met	Lys	Arg	Asp	Val	Lys	Val	Thr	Pro	Gly	Thr	Lys	His	Thr	Glu	
				2110					2115					2120		
GAA	AGA	CCC	AAA	GTC	CAG	GTA	ATT	CAA	GCA	GCG	GAG	CCA	TTG	GCG	ACC	6497
Glu	Arg	Pro	Lys	Val	Gln	Val	Ile	Gln	Ala	Ala	Glu	Pro	Leu	Ala	Thr	
			2125					2130					2135			
GCT	TAC	CTG	TGC	GGC	ATC	CAC	AGG	GAA	TTA	GTA	AGG	AGA	CTA	AAT	GCT	6545
Ala	Tyr	Leu	Cys	Gly	Ile	His	Arg	Glu	Leu	Val	Arg	Arg	Leu	Asn	Ala	
		2140					2145					2150				

GTG TTA CGC CCT AAC GTG CAC ACA TTG TTT GAT ATG TCG GCC GAA GAC Val Leu Arg Pro Asn Val His Thr Leu Phe Asp Met Ser Ala Glu Asp 2155 2160 2165	6593
TTT GAC GCG ATC ATC GCC TCT CAC TTC CAC CCA GGA GAC CCG GTT CTA Phe Asp Ala Ile Ile Ala Ser His Phe His Pro Gly Asp Pro Val Leu 2170 2175 2180 2185	6641
GAG ACG GAC ATT GCA TCA TTC GAC AAA AGC CAG GAC GAC TCC TTG GCT Glu Thr Asp Ile Ala Ser Phe Asp Lys Ser Gln Asp Asp Ser Leu Ala 2190 2195 2200	6689
CTT ACA GGT TTA ATG ATC CTC GAA GAT CTA GGG GTG GAT CAG TAC CTG Leu Thr Gly Leu Met Ile Leu Glu Asp Leu Gly Val Asp Gln Tyr Leu 2205 2210 2215	6737
CTG GAC TTG ATC GAG GCA GCC TTT GGG GAA ATA TCC AGC TGT CAC CTA Leu Asp Leu Ile Glu Ala Ala Phe Gly Glu Ile Ser Ser Cys His Leu 2220 2225 2230	6785
CCA ACT GGC ACG CGC TTC AAG TTC GGA GCT ATG ATG AAA TCG GGC ATG Pro Thr Gly Thr Arg Phe Lys Phe Gly Ala Met Met Lys Ser Gly Met 2235 2240 2245	6833
TTT CTG ACT TTG TTT ATT AAC ACT GTT TTG AAC ATC ACC ATA GCA AGC Phe Leu Thr Leu Phe Ile Asn Thr Val Leu Asn Ile Thr Ile Ala Ser 2250 2255 2260 2265	6881
AGG GTA CTG GAG CAG AGA CTC ACT GAC TCC GCC TGT GCG GCC TTC ATC Arg Val Leu Glu Gln Arg Leu Thr Asp Ser Ala Cys Ala Ala Phe Ile 2270 2275 2280	6929
GGC GAC GAC AAC ATC GTT CAC GGA GTG ATC TCC GAC AAG CTG ATG GCG Gly Asp Asp Asn Ile Val His Gly Val Ile Ser Asp Lys Leu Met Ala 2285 2290 2295	6977
GAG AGG TGC GCG TCG TGG GTC AAC ATG GAG GTG AAG ATC ATT GAC GCT Glu Arg Cys Ala Ser Trp Val Asn Met Glu Val Lys Ile Ile Asp Ala 2300 2305 2310	7025
GTC ATG GGC GAA AAA CCC CCA TAT TTT TGT GGG GGA TTC ATA GTT TTT Val Met Gly Glu Lys Pro Pro Tyr Phe Cys Gly Gly Phe Ile Val Phe 2315 2320 2325	7073
GAC AGC GTC ACA CAG ACC GCC TGC CGT GTT TCA GAC CCA CTT AAG CGC Asp Ser Val Thr Gln Thr Ala Cys Arg Val Ser Asp Pro Leu Lys Arg 2330 2335 2340 2345	7121
CTG TTC AAG TTG GGT AAG CCG CTA ACA GCT GAA GAC AAG CAG GAC GAA Leu Phe Lys Leu Gly Lys Pro Leu Thr Ala Glu Asp Lys Gln Asp Glu 2350 2355 2360	7169

GAC AGG CGA CGA GCA CTG AGT GAC GAG GTT AGC AAG TGG TTC CGG ACA	7217
Asp Arg Arg Arg Ala Leu Ser Asp Glu Val Ser Lys Trp Phe Arg Thr	
2365 2370 2375	
GGC TTG GGG GCC GAA CTG GAG GTG GCA CTA ACA TCT AGG TAT GAG GTA	7265
Gly Leu Gly Ala Glu Leu Glu Val Ala Leu Thr Ser Arg Tyr Glu Val	
2380 2385 2390	
GAG GGC TGC AAA AGT ATC CTC ATA GCC ATG ACC ACC TTG GCG AGG GAC	7313
Glu Gly Cys Lys Ser Ile Leu Ile Ala Met Thr Thr Leu Ala Arg Asp	
2395 2400 2405	
ATT AAG GCG TTT AAG AAA TTG AGA GGA CCT GTT ATA CAC CTC TAC GGC	7361
Ile Lys Ala Phe Lys Lys Leu Arg Gly Pro Val Ile His Leu Tyr Gly	
2410 2415 2420 2425	
GGT CCT AGA TTG GTG CGT TAATACACAG AATTCTGATT ATAGCGCACT	7409
Gly Pro Arg Leu Val Arg	
2430	
ATTATAGCAC C ATG AAT TAC ATC CCT ACG CAA ACG TTT TAC GGC CGC CGG	7459
Met Asn Tyr Ile Pro Thr Gln Thr Phe Tyr Gly Arg Arg	
1 5 10	
TGG CGC CCG CGC CCG GCG GCC CGT CCT TGG CCG TTG CAG GCC ACT CCG	7507
Trp Arg Pro Arg Pro Ala Ala Arg Pro Trp Pro Leu Gln Ala Thr Pro	
15 20 25	
GTG GCT CCC GTC GTC CCC GAC TTC CAG GCC CAG CAG ATG CAG CAA CTC	7555
Val Ala Pro Val Val Pro Asp Phe Gln Ala Gln Gln Met Gln Gln Leu	
30 35 40 45	
ATC AGC GCC GTA AAT GCG CTG ACA ATG AGA CAG AAC GCA ATT GCT CCT	7603
Ile Ser Ala Val Asn Ala Leu Thr Met Arg Gln Asn Ala Ile Ala Pro	
50 55 60	
GCT AGG CCT CCC AAA CCA AAG AAG AAG AAG ACA ACC AAA CCA AAG CCG	7651
Ala Arg Pro Pro Lys Pro Lys Lys Lys Lys Thr Thr Lys Pro Lys Pro	
65 70 75	
AAA ACG CAG CCC AAG AAG ATC AAC GGA AAA ACG CAG CAG CAA AAG AAG	7699
Lys Thr Gln Pro Lys Lys Ile Asn Gly Lys Thr Gln Gln Gln Lys Lys	
80 85 90	
AAA GAC AAG CAA GCC GAC AAG AAG AAG AAG AAA CCC GGA AAA AGA GAA	7747
Lys Asp Lys Gln Ala Asp Lys Lys Lys Lys Lys Pro Gly Lys Arg Glu	
95 100 105	
AGA ATG TGC ATG AAG ATT GAA AAT GAC TGT ATC TTC GAA GTC AAA CAC	7795
Arg Met Cys Met Lys Ile Glu Asn Asp Cys Ile Phe Glu Val Lys His	
110 115 120 125	

GAA	GGA	AAG	GTC	ACT	GGG	TAC	GCC	TGC	CTG	GTG	GGC	GAC	AAA	GTC	ATG	7843
Glu	Gly	Lys	Val	Thr	Gly	Tyr	Ala	Cys	Leu	Val	Gly	Asp	Lys	Val	Met	
			130						135					140		
AAA	CCT	GCC	CAC	GTG	AAA	GGA	GTC	ATC	GAC	AAC	GCG	GAC	CTG	GCA	AAG	7891
Lys	Pro	Ala	His	Val	Lys	Gly	Val	Ile	Asp	Asn	Ala	Asp	Leu	Ala	Lys	
			145					150					155			
CTA	GCT	TTC	AAG	AAA	TCG	AGC	AAG	TAT	GAC	CTT	GAG	TGT	GCC	CAG	ATA	7939
Leu	Ala	Phe	Lys	Lys	Ser	Ser	Lys	Tyr	Asp	Leu	Glu	Cys	Ala	Gln	Ile	
		160					165					170				
CCA	GTT	CAC	ATG	AGG	TCG	GAT	GCC	TCA	AAG	TAC	ACG	CAT	GAG	AAG	CCC	7987
Pro	Val	His	Met	Arg	Ser	Asp	Ala	Ser	Lys	Tyr	Thr	His	Glu	Lys	Pro	
	175					180					185					
GAG	GGA	CAC	TAT	AAC	TGG	CAC	CAC	GGG	GCT	GTT	CAG	TAC	AGC	GGA	GGT	8035
Glu	Gly	His	Tyr	Asn	Trp	His	His	Gly	Ala	Val	Gln	Tyr	Ser	Gly	Gly	
190					195					200					205	
AGG	TTC	ACT	ATA	CCG	ACA	GGA	GCG	GGC	AAA	CCG	GGA	GAC	AGT	GGC	CGG	8083
Arg	Phe	Thr	Ile	Pro	Thr	Gly	Ala	Gly	Lys	Pro	Gly	Asp	Ser	Gly	Arg	
			210						215					220		
CCC	ATC	TTT	GAC	AAC	AAG	GGG	AGG	GTA	GTC	GCT	ATC	GTC	CTG	GGC	GGG	8131
Pro	Ile	Phe	Asp	Asn	Lys	Gly	Arg	Val	Val	Ala	Ile	Val	Leu	Gly	Gly	
			225					230					235			
GGC	AAC	GAG	GGC	TCA	CGC	ACA	GCA	CTG	TCG	GTG	GTC	ACC	TGG	AAC	AAA	8179
Ala	Asn	Glu	Gly	Ser	Arg	Thr	Ala	Leu	Ser	Val	Val	Thr	Trp	Asn	Lys	
	240						245					250				
GAT	ATG	GTG	ACT	AGA	GTG	ACC	CCC	GAG	GGG	TCC	GAA	GAG	TGG	TCC	GCC	8227
Asp	Met	Val	Thr	Arg	Val	Thr	Pro	Glu	Gly	Ser	Glu	Glu	Trp	Ser	Ala	
	255					260					265					
CCG	CTG	ATT	ACT	GCC	ATG	TGT	GTC	CTT	GCC	AAT	GCT	ACC	TTC	CCG	TGC	8275
Pro	Leu	Ile	Thr	Ala	Met	Cys	Val	Leu	Ala	Asn	Ala	Thr	Phe	Pro	Cys	
	270				275					280					285	
TTC	CAG	CCC	CCG	TGT	GTA	CCT	TGC	TGC	TAT	GAA	AAC	AAC	GCA	GAG	GCC	8323
Phe	Gln	Pro	Pro	Cys	Val	Pro	Cys	Cys	Tyr	Glu	Asn	Asn	Ala	Glu	Ala	
			290						295					300		
ACA	CTA	CGG	ATG	CTC	GAG	GAT	AAC	GTG	GAT	AGG	CCA	GGG	TAC	TAC	GAC	8371
Thr	Leu	Arg	Met	Leu	Glu	Asp	Asn	Val	Asp	Arg	Pro	Gly	Tyr	Tyr	Asp	
		305						310					315			
CTC	CTT	CAG	GCA	GCC	TTG	ACG	TGC	CGA	AAC	GGA	ACA	AGA	CAC	CGG	CGC	8419
Leu	Leu	Gln	Ala	Ala	Leu	Thr	Cys	Arg	Asn	Gly	Thr	Arg	His	Arg	Arg	
		320					325					330				

AGC Ser 335	GTG Val	TCG Ser	CAA Gln	CAC His	TTC Phe	AAC Asn 340	GTG Val	TAT Tyr	AAG Lys	GCT Ala	ACA Thr 345	CGC Arg	CCT Pro	TAC Tyr	ATC Ile	8467
GCG Ala 350	TAC Tyr	TGC Cys	GCC Ala	GAC Asp	TGC Cys 355	GGA Gly	GCA Ala	GGG Gly	CAC His	TCG Ser 360	TGT Cys	CAT His	AGC Ser	CCC Pro	GTA Val 365	8515
GCA Ala	ATT Ile	GAA Glu	GCG Ala	GTC Val 370	AGG Arg	TCC Ser	GAA Glu	GCT Ala	ACC Thr 375	GAC Asp	GGG Gly	ATG Met	CTG Leu	AAG Lys 380	ATT Ile	8563
CAG Gln	TTC Phe	TCG Ser	GCA Ala 385	CAA Gln	ATT Ile	GGC Gly	ATA Ile	GAT Asp 390	AAG Lys	AGT Ser	GAC Asp	AAT Asn 395	CAT His	GAC Asp	TAC Tyr	8611
ACG Thr	AAG Lys	ATA Ile 400	AGG Arg	TAC Tyr	GCA Ala	GAC Asp	GGG Gly 405	CAC His	GCC Ala	ATT Ile	GAG Glu	AAT Asn 410	GCC Ala	GTC Val	CGG Arg	8659
TCA Ser 415	TCT Ser	TTG Leu	AAG Lys	GTA Val	GCC Ala	ACC Thr 420	TCC Ser	GGA Gly	GAC Asp	TGT Cys	TTC Phe 425	GTC Val	CAT His	GGC Gly	ACA Thr	8707
ATG Met 430	GGA Gly	CAT His	TTC Phe	ATA Ile	CTG Leu 435	GCA Ala	AAG Lys	TGC Cys	CCA Pro	CCG Pro 440	GGT Gly	GAA Glu	TTC Phe	CTG Leu	CAG Gln 445	8755
GTC Val	TCG Ser	ATC Ile	CAG Gln	GAC Asp 450	ACC Thr	AGA Arg	AAC Asn	GCG Ala	GTC Val 455	CGT Arg	GCC Ala	TGC Cys	AGA Arg	ATA Ile 460	CAA Gln	8803
TAT Tyr	CAT His	CAT His	GAC Asp 465	CCT Pro	CAA Gln	CCG Pro	GTG Val	GGT Gly 470	AGA Arg	GAA Glu	AAA Lys	TTT Phe	ACA Thr 475	ATT Ile	AGA Arg	8851
CCA Pro	CAC His	TAT Tyr 480	GGA Gly	AAA Lys	GAG Glu	ATC Ile	CCT Pro 485	TGC Cys	ACC Thr	ACT Thr	TAT Tyr	CAA Gln 490	CAG Gln	ACC Thr	ACA Thr	8899
GCG Ala 495	AAG Lys	ACC Thr	GTG Val	GAG Glu	GAA Glu	ATC Ile 500	GAC Asp	ATG Met	CAT His	ATG Met	CCG Pro 505	CCA Pro	GAT Asp	ACG Thr	CCG Pro	8947
GAC Asp 510	AGG Arg	ACG Thr	TTG Leu	CTA Leu	TCA Ser 515	CAG Gln	CAA Gln	TCT Ser	GGC Gly	AAT Asn 520	GTA Val	AAG Lys	ATC Ile	ACA Thr	GTC Val 525	8995
GGA Gly	GGA Gly	AAG Lys	AAG Lys	GTG Val 530	AAA Lys	TAC Tyr	AAC Asn	TGC Cys	ACC Thr 535	TGT Cys	GGA Gly	ACC Thr	GGA Gly	AAC Asn 540	GTT Val	9043

GGC	ACT	ACT	AAT	TCG	GAC	ATG	ACG	ATC	AAC	ACG	TGT	CTA	ATA	GAG	CAG	9091
Gly	Thr	Thr	Asn	Ser	Asp	Met	Thr	Ile	Asn	Thr	Cys	Leu	Ile	Glu	Gln	
			545					550					555			
TGC	CAC	GTC	TCA	GTG	ACG	GAC	CAT	AAG	AAA	TGG	CAG	TTC	AAC	TCA	CCT	9139
Cys	His	Val	Ser	Val	Thr	Asp	His	Lys	Lys	Trp	Gln	Phe	Asn	Ser	Pro	
		560					565					570				
TTC	GTC	CCG	AGA	GCC	GAC	GAA	CCG	GCT	AGA	AAA	GGC	AAA	GTC	CAT	ATC	9187
Phe	Val	Pro	Arg	Ala	Asp	Glu	Pro	Ala	Arg	Lys	Gly	Lys	Val	His	Ile	
	575					580					585					
CCA	TTC	CCG	TTG	GAC	AAC	ATC	ACA	TGC	AGA	GTT	CCA	ATG	GCG	CGC	GAA	9235
Pro	Phe	Pro	Leu	Asp	Asn	Ile	Thr	Cys	Arg	Val	Pro	Met	Ala	Arg	Glu	
590					595					600					605	
CCA	ACC	GTC	ATC	CAC	GGC	AAA	AGA	GAA	GTG	ACA	CTG	CAC	CTT	CAC	CCA	9283
Pro	Thr	Val	Ile	His	Gly	Lys	Arg	Glu	Val	Thr	Leu	His	Leu	His	Pro	
				610					615					620		
GAT	CAT	CCC	ACG	CTC	TTT	TCC	TAC	CGC	ACA	CTG	GGT	GAG	GAC	CCG	CAG	9331
Asp	His	Pro	Thr	Leu	Phe	Ser	Tyr	Arg	Thr	Leu	Gly	Glu	Asp	Pro	Gln	
			625					630					635			
TAT	CAC	GAG	GAA	TGG	GTG	ACA	GCG	GCG	GTG	GAA	CGG	ACC	ATA	CCC	GTA	9379
Tyr	His	Glu	Glu	Trp	Val	Thr	Ala	Ala	Val	Glu	Arg	Thr	Ile	Pro	Val	
		640					645					650				
CCA	GTG	GAC	GGG	ATG	GAG	TAC	CAC	TGG	GGA	AAC	AAC	GAC	CCA	GTG	AGG	9427
Pro	Val	Asp	Gly	Met	Glu	Tyr	His	Trp	Gly	Asn	Asn	Asp	Pro	Val	Arg	
	655					660					665					
CTT	TGG	TCT	CAA	CTC	ACC	ACT	GAA	GGG	AAA	CCG	CAC	GGC	TGG	CCG	CAT	9475
Leu	Trp	Ser	Gln	Leu	Thr	Thr	Glu	Gly	Lys	Pro	His	Gly	Trp	Pro	His	
670					675					680					685	
CAG	ATC	GTA	CAG	TAC	TAC	TAT	GGG	CTT	TAC	CCG	GCC	GCT	ACA	GTA	TCC	9523
Gln	Ile	Val	Gln	Tyr	Tyr	Tyr	Gly	Leu	Tyr	Pro	Ala	Ala	Thr	Val	Ser	
				690					695					700		
GCG	GTC	GTC	GGG	ATG	AGC	TTA	CTG	GCG	TTG	ATA	TCG	ATC	TTC	GCG	TCG	9571
Ala	Val	Val	Gly	Met	Ser	Leu	Leu	Ala	Leu	Ile	Ser	Ile	Phe	Ala	Ser	
			705					710					715			
TGC	TAC	ATG	CTG	GTT	GCG	GCC	CGC	AGT	AAG	TGC	TTG	ACC	CCT	TAT	GCT	9619
Cys	Tyr	Met	Leu	Val	Ala	Ala	Arg	Ser	Lys	Cys	Leu	Thr	Pro	Tyr	Ala	
		720					725					730				
TTA	ACA	CCA	GGA	GCT	GCA	GTT	CCG	TGG	ACG	CTG	GGG	ATA	CTC	TGC	TGC	9667
Leu	Thr	Pro	Gly	Ala	Ala	Val	Pro	Trp	Thr	Leu	Gly	Ile	Leu	Cys	Cys	
	735					740					745					

GCC	CCG	CGG	GCG	CAC	GCA	GCT	AGT	GTG	GCA	GAG	ACT	ATG	GCC	TAC	TTG	9715
Ala	Pro	Arg	Ala	His	Ala	Ala	Ser	Val	Ala	Glu	Thr	Met	Ala	Tyr	Leu	
750					755				760						765	
TGG	GAC	CAA	AAC	CAA	GCG	TTG	TTC	TGG	TTG	GAG	TTT	GCG	GCC	CCT	GTT	9763
Trp	Asp	Gln	Asn	Gln	Ala	Leu	Phe	Trp	Leu	Glu	Phe	Ala	Ala	Pro	Val	
				770					775					780		
GCC	TGC	ATC	CTC	ATC	ATC	ACG	TAT	TGC	CTC	AGA	AAC	GTG	CTG	TGT	TGC	9811
Ala	Cys	Ile	Leu	Ile	Ile	Thr	Tyr	Cys	Leu	Arg	Asn	Val	Leu	Cys	Cys	
			785					790					795			
TGT	AAG	AGC	CTT	TCT	TTT	TTA	GTG	CTA	CTG	AGC	CTC	GGG	GCA	ACC	GCC	9859
Cys	Lys	Ser	Leu	Ser	Phe	Leu	Val	Leu	Leu	Ser	Leu	Gly	Ala	Thr	Ala	
		800					805					810				
AGA	GCT	TAC	GAA	CAT	TCG	ACA	GTA	ATG	CCG	AAC	GTG	GTG	GGG	TTC	CCG	9907
Arg	Ala	Tyr	Glu	His	Ser	Thr	Val	Met	Pro	Asn	Val	Val	Gly	Phe	Pro	
815						820					825					
TAT	AAG	GCT	CAC	ATT	GAA	AGG	CCA	GGA	TAT	AGC	CCC	CTC	ACT	TTG	CAG	9955
Tyr	Lys	Ala	His	Ile	Glu	Arg	Pro	Gly	Tyr	Ser	Pro	Leu	Thr	Leu	Gln	
830					835					840					845	
ATG	CAG	GTT	GTT	GAA	ACC	AGC	CTC	GAA	CCA	ACC	CTT	AAT	TTG	GAA	TAC	10003
Met	Gln	Val	Val	Glu	Thr	Ser	Leu	Glu	Pro	Thr	Leu	Asn	Leu	Glu	Tyr	
				850					855					860		
ATA	ACC	TGT	GAG	TAC	AAG	ACG	GTC	GTC	CCG	TCG	CCG	TAC	GTG	AAG	TGC	10051
Ile	Thr	Cys	Glu	Tyr	Lys	Thr	Val	Val	Pro	Ser	Pro	Tyr	Val	Lys	Cys	
			865					870					875			
TGC	GGC	GCC	TCA	GAG	TGC	TCC	ACT	AAA	GAG	AAG	CCT	GAC	TAC	CAA	TGC	10099
Cys	Gly	Ala	Ser	Glu	Cys	Ser	Thr	Lys	Glu	Lys	Pro	Asp	Tyr	Gln	Cys	
		880					885					890				
AAG	GTT	TAC	ACA	GGC	GTG	TAC	CCG	TTC	ATG	TGG	GGA	GGG	GCA	TAT	TGC	10147
Lys	Val	Tyr	Thr	Gly	Val	Tyr	Pro	Phe	Met	Trp	Gly	Gly	Ala	Tyr	Cys	
	895					900					905					
TTC	TGC	GAC	TCA	GAA	AAC	ACG	CAA	CTC	AGC	GAG	GCG	TAC	GTC	GAT	CGA	10195
Phe	Cys	Asp	Ser	Glu	Asn	Thr	Gln	Leu	Ser	Glu	Ala	Tyr	Val	Asp	Arg	
910					915					920					925	
TCG	GAC	GTA	TGC	AGG	CAT	GAT	CAC	GCA	TCT	GCT	TAC	AAA	GCC	CAT	ACA	10243
Ser	Asp	Val	Cys	Arg	His	Asp	His	Ala	Ser	Ala	Tyr	Lys	Ala	His	Thr	
				930					935					940		
GCA	TCG	CTG	AAG	GCC	AAA	GTG	AGG	GTT	ATG	TAC	GGC	AAC	GTA	AAC	CAG	10291
Ala	Ser	Leu	Lys	Ala	Lys	Val	Arg	Val	Met	Tyr	Gly	Asn	Val	Asn	Gln	
			945					950					955			

ACT Thr	GTG Val	GAT Asp	GTT Val	TAC Tyr	GTG Val	AAC Asn	GGA Gly	GAC Asp	CAT His	GCC Ala	GTC Val	ACG Thr	ATA Ile	GGG Gly	GGT Gly	10339
	960						965					970				
ACT Thr	CAG Gln	TTC Phe	ATA Ile	TTC Phe	GGG Gly	CCG Pro	CTG Leu	TCA Ser	TCG Ser	GCC Ala	TGG Trp	ACC Thr	CCG Pro	TTC Phe	GAC Asp	10387
	975					980					985					
AAC Asn	AAG Lys	ATA Ile	GTC Val	GTG Val	TAC Tyr	AAA Lys	GAC Asp	GAA Glu	GTG Val	TTC Phe	AAT Asn	CAG Gln	GAC Asp	TTC Phe	CCG Pro	10435
	990				995					1000					1005	
CCG Pro	TAC Tyr	GGA Gly	TCT Ser	GGG Gly	CAA Gln	CCA Pro	GGG Gly	CGC Arg	TTC Phe	GGC Gly	GAC Asp	ATC Ile	CAA Gln	AGC Ser	AGA Arg	10483
				1010					1015					1020		
ACA Thr	GTG Val	GAG Glu	AGT Ser	AAC Asn	GAC Asp	CTG Leu	TAC Tyr	GCG Ala	AAC Asn	ACG Thr	GCA Ala	CTG Leu	AAG Lys	CTG Leu	GCA Ala	10531
				1025				1030					1035			
CGC Arg	CCT Pro	TCA Ser	CCC Pro	GGC Gly	ATG Met	GTC Val	CAT His	GTA Val	CCG Pro	TAC Tyr	ACA Thr	CAG Gln	ACA Thr	CCT Pro	TCA Ser	10579
		1040					1045					1050				
GGG Gly	TTC Phe	AAA Lys	TAT Tyr	TGG Trp	CTA Leu	AAG Lys	GAA Glu	AAA Lys	GGG Gly	ACA Thr	GCC Ala	CTA Leu	AAT Asn	ACG Thr	AAG Lys	10627
	1055					1060					1065					
GCT Ala	CCT Pro	TTT Phe	GGC Gly	TGC Cys	CAA Gln	ATC Ile	AAA Lys	ACG Thr	AAC Asn	CCT Pro	GTC Val	AGG Arg	GCC Ala	ATG Met	AAC Asn	10675
	1070				1075					1080					1085	
TGC Cys	GCC Ala	GTG Val	GGA Gly	AAC Asn	ATC Ile	CCT Pro	GTC Val	TCC Ser	ATG Met	AAT Asn	TTG Leu	CCT Pro	GAC Asp	AGC Ser	GCC Ala	10723
				1090				1095						1100		
TTT Phe	ACC Thr	CGC Arg	ATT Ile	GTC Val	GAG Glu	GCG Ala	CCG Pro	ACC Thr	ATC Ile	ATT Ile	GAC Asp	CTG Leu	ACT Thr	TGC Cys	ACA Thr	10771
			1105					1110					1115			
GTG Val	GCT Ala	ACC Thr	TGT Cys	ACG Thr	CAC His	TCC Ser	TCG Ser	GAT Asp	TTC Phe	GGC Gly	GGC Gly	GTC Val	TTG Leu	ACA Thr	CTG Leu	10819
		1120					1125					1130				
ACG Thr	TAC Tyr	AAG Lys	ACC Thr	AAC Asn	AAG Lys	AAC Asn	GGG Gly	GAC Asp	TGC Cys	TCT Ser	GTA Val	CAC His	TCG Ser	CAC His	TCT Ser	10867
	1135					1140					1145					
AAC Asn	GTA Val	GCT Ala	ACT Thr	CTA Leu	CAG Gln	GAG Glu	GCC Ala	ACA Thr	GCA Ala	AAA Lys	GTG Val	AAG Lys	ACA Thr	GCA Ala	GGT Gly	10915
	1150				1155					1160					1165	

AAG GTG ACC TTA CAC TTC TCC ACG GCA AGC GCA TCA CCT TCT TTT GTG	10963
Lys Val Thr Leu His Phe Ser Thr Ala Ser Ala Ser Pro Ser Phe Val	
1170 1175 1180	
GTG TCG CTA TGC AGT GCT AGG GCC ACC TGT TCA GCG TCG TGT GAG CCC	11011
Val Ser Leu Cys Ser Ala Arg Ala Thr Cys Ser Ala Ser Cys Glu Pro	
1185 1190 1195	
CCG AAA GAC CAC ATA GTC CCA TAT GCG GCT AGC CAC AGT AAC GTA GTG	11059
Pro Lys Asp His Ile Val Pro Tyr Ala Ala Ser His Ser Asn Val Val	
1200 1205 1210	
TTT CCA GAC ATG TCG GGC ACC GCA CTA TCA TGG GTG CAG AAA ATC TCG	11107
Phe Pro Asp Met Ser Gly Thr Ala Leu Ser Trp Val Gln Lys Ile Ser	
1215 1220 1225	
GGT GGT CTG GGG GCC TTC GCA ATC GGC GCT ATC CTG GTG CTG GTT GTG	11155
Gly Gly Leu Gly Ala Phe Ala Ile Gly Ala Ile Leu Val Leu Val Val	
1230 1235 1240 1245	
CGTC ACT TGC ATT GGG CTC CGC AGA TAAGTTAGGG TAGGCAATGG CATTGATATA	11209
Val Thr Cys Ile Gly Leu Arg Arg	
1250	
GCAAGAAAAT TGAAAACAGA AAAAGTTAGG GTAAGCAATG GCATATAACC ATAAGTGTAT	11269
AACTTGTAAC AAAGCGCAAC AAGACCTGCG CAATTGGCCC CGTGGTCCGC CTCACGGAAA	11329
CTCGGGGCAA CTCATATTGA CACATTAATT GGCAATAATT GGAAGCTTAC ATAAGCTTAA	11389
TTCGACGAAT AATTGGATTT TTATTTTATT TTGCAATTGG TTTTAAATAT TTCCAAAAAA	11449
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	11509
AAACTAG	11517

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2431 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ala	Ala	Lys	Val	His	Val	Asp	Ile	Glu	Ala	Asp	Ser	Pro	Phe	Ile
1				5					10					15	
Lys	Ser	Leu	Gln	Lys	Ala	Phe	Pro	Ser	Phe	Glu	Val	Glu	Ser	Leu	Gln

Ala	Val	Thr	Tyr	His	Ala	Glu	Gly	Phe	Leu	Val	Cys	Lys	Thr	Thr	Asp	305	310	315	320
Thr	Val	Lys	Gly	Glu	Arg	Val	Ser	Phe	Pro	Val	Cys	Thr	Tyr	Val	Pro	325	330	335	
Ser	Thr	Ile	Cys	Asp	Gln	Met	Thr	Gly	Ile	Leu	Ala	Thr	Asp	Val	Thr	340	345	350	
Pro	Glu	Asp	Ala	Gln	Lys	Leu	Leu	Val	Gly	Leu	Asn	Gln	Arg	Ile	Val	355	360	365	
Val	Asn	Gly	Arg	Thr	Gln	Arg	Asn	Thr	Asn	Thr	Met	Lys	Asn	Tyr	Leu	370	375	380	
Leu	Pro	Ile	Val	Ala	Val	Ala	Phe	Ser	Lys	Trp	Ala	Arg	Glu	Tyr	Lys	385	390	395	400
Ala	Asp	Leu	Asp	Asp	Glu	Lys	Pro	Leu	Gly	Val	Arg	Glu	Arg	Ser	Leu	405	410	415	
Thr	Cys	Cys	Cys	Leu	Trp	Ala	Phe	Lys	Thr	Arg	Lys	Met	His	Thr	Met	420	425	430	
Tyr	Lys	Lys	Pro	Asp	Thr	Gln	Thr	Ile	Val	Lys	Val	Pro	Ser	Glu	Phe	435	440	445	
Asn	Ser	Phe	Val	Ile	Pro	Ser	Leu	Trp	Ser	Thr	Gly	Leu	Ala	Ile	Pro	450	455	460	
Val	Arg	Ser	Arg	Ile	Lys	Met	Leu	Leu	Ala	Lys	Lys	Thr	Lys	Arg	Glu	465	470	475	480
Leu	Ile	Pro	Val	Leu	Asp	Ala	Ser	Ser	Ala	Arg	Asp	Ala	Glu	Gln	Glu	485	490	495	
Glu	Lys	Glu	Arg	Leu	Glu	Ala	Glu	Leu	Thr	Arg	Glu	Ala	Leu	Pro	Pro	500	505	510	
Leu	Val	Pro	Ile	Ala	Pro	Ala	Glu	Thr	Gly	Val	Val	Asp	Val	Asp	Val	515	520	525	
Glu	Glu	Leu	Glu	Tyr	His	Ala	Gly	Ala	Gly	Val	Val	Glu	Thr	Pro	Arg	530	535	540	
Ser	Ala	Leu	Lys	Val	Thr	Ala	Gln	Pro	Asn	Asp	Val	Leu	Leu	Gly	Asn	545	550	555	560
Tyr	Val	Val	Leu	Ser	Pro	Gln	Thr	Val	Leu	Lys	Ser	Ser	Lys	Leu	Ala	565	570	575	

Pro	Val	His	Pro	Leu	Ala	Glu	Gln	Val	Lys	Ile	Ile	Thr	His	Asn	Gly
			580					585					590		
Arg	Ala	Gly	Gly	Tyr	Gln	Val	Asp	Gly	Tyr	Asp	Gly	Arg	Val	Leu	Leu
		595					600					605			
Pro	Cys	Gly	Ser	Ala	Ile	Pro	Val	Pro	Glu	Phe	Gln	Ala	Leu	Ser	Glu
	610					615					620				
Ser	Ala	Thr	Met	Val	Tyr	Asn	Glu	Arg	Glu	Phe	Val	Asn	Arg	Lys	Leu
625					630					635					640
Tyr	His	Ile	Ala	Val	His	Gly	Pro	Ser	Leu	Asn	Thr	Asp	Glu	Glu	Asn
				645					650					655	
Tyr	Glu	Lys	Val	Arg	Ala	Glu	Arg	Thr	Asp	Ala	Glu	Tyr	Val	Phe	Asp
			660					665					670		
Val	Asp	Lys	Lys	Cys	Cys	Val	Lys	Arg	Glu	Glu	Ala	Ser	Gly	Leu	Val
		675					680					685			
Leu	Val	Gly	Glu	Leu	Thr	Asn	Pro	Pro	Phe	His	Glu	Phe	Ala	Tyr	Glu
	690					695					700				
Gly	Leu	Lys	Ile	Arg	Pro	Ser	Ala	Pro	Tyr	Lys	Thr	Thr	Val	Val	Gly
705					710					715					720
Val	Phe	Gly	Val	Pro	Gly	Ser	Gly	Lys	Ser	Ala	Ile	Ile	Lys	Ser	Leu
				725					730					735	
Val	Thr	Lys	His	Asp	Leu	Val	Thr	Ser	Gly	Lys	Lys	Glu	Asn	Cys	Gln
			740					745					750		
Glu	Ile	Val	Asn	Asp	Val	Lys	Lys	His	Arg	Gly	Lys	Gly	Thr	Ser	Arg
		755					760					765			
Glu	Asn	Ser	Asp	Ser	Ile	Leu	Leu	Asn	Gly	Cys	Arg	Arg	Ala	Val	Asp
	770					775					780				
Ile	Leu	Tyr	Val	Asp	Glu	Ala	Phe	Ala	Cys	His	Ser	Gly	Thr	Leu	Leu
785					790					795					800
Ala	Leu	Ile	Ala	Leu	Val	Lys	Pro	Arg	Ser	Lys	Val	Val	Leu	Cys	Gly
				805					810					815	
Asp	Pro	Lys	Gln	Cys	Gly	Phe	Phe	Asn	Met	Met	Gln	Leu	Lys	Val	Asn
			820					825					830		
Phe	Asn	His	Asn	Ile	Cys	Thr	Glu	Val	Cys	His	Lys	Ser	Ile	Ser	Arg
		835					840					845			

Arg	Cys	Thr	Arg	Pro	Val	Thr	Ala	Ile	Val	Ser	Thr	Leu	His	Tyr	Gly	
	850						855				860					
Gly	Lys	Met	Arg	Thr	Thr	Asn	Pro	Cys	Asn	Lys	Pro	Ile	Ile	Ile	Asp	
865					870					875					880	
Thr	Thr	Gly	Gln	Thr	Lys	Pro	Lys	Pro	Gly	Asp	Ile	Val	Leu	Thr	Cys	
				885						890				895		
Phe	Arg	Gly	Trp	Ala	Lys	Gln	Leu	Gln	Leu	Asp	Tyr	Arg	Gly	His	Glu	
			900					905					910			
Val	Met	Thr	Ala	Ala	Ala	Ser	Gln	Gly	Leu	Thr	Arg	Lys	Gly	Val	Tyr	
		915					920					925				
Ala	Val	Arg	Gln	Lys	Val	Asn	Glu	Asn	Pro	Leu	Tyr	Ala	Pro	Ala	Ser	
						935					940					
Glu	His	Val	Asn	Val	Leu	Leu	Thr	Arg	Thr	Glu	Asp	Arg	Leu	Val	Trp	
945					950					955					960	
Lys	Thr	Leu	Ala	Gly	Asp	Pro	Trp	Ile	Lys	Val	Leu	Ser	Asn	Ile	Pro	
				965						970				975		
Gln	Gly	Asn	Phe	Thr	Ala	Thr	Leu	Glu	Glu	Trp	Gln	Glu	Glu	His	Asp	
			980					985						990		
Lys	Ile	Met	Lys	Val	Ile	Glu	Gly	Pro	Ala	Ala	Pro	Val	Asp	Ala	Phe	
		995					1000					1005				
Gln	Asn	Lys	Ala	Asn	Val	Cys	Trp	Ala	Lys	Ser	Leu	Val	Pro	Val	Leu	
	1010					1015					1020					
Asp	Thr	Ala	Gly	Ile	Arg	Leu	Thr	Ala	Glu	Glu	Trp	Ser	Thr	Ile	Ile	
1025					1030					1035					1040	
Thr	Ala	Phe	Lys	Glu	Asp	Arg	Ala	Tyr	Ser	Pro	Val	Val	Ala	Leu	Asn	
				1045					1050					1055		
Glu	Ile	Cys	Thr	Lys	Tyr	Tyr	Gly	Val	Asp	Leu	Asp	Ser	Gly	Leu	Phe	
			1060					1065					1070			
Ser	Ala	Pro	Lys	Val	Ser	Leu	Tyr	Tyr	Glu	Asn	Asn	His	Trp	Asp	Asn	
		1075					1080					1085				
Arg	Pro	Gly	Gly	Arg	Met	Tyr	Gly	Phe	Asn	Ala	Ala	Thr	Ala	Ala	Arg	
	1090					1095					1100					
Leu	Glu	Ala	Arg	His	Thr	Phe	Leu	Lys	Gly	Gln	Trp	His	Thr	Gly	Lys	
1105					1110					1115					1120	

Gln Ala Val Ile Ala Glu Arg Lys Ile Gln Pro Leu Ser Val Leu Asp
 1125 1130 1135
 Asn Val Ile Pro Ile Asn Arg Arg Leu Pro His Ala Leu Val Ala Glu
 1140 1145 1150
 Tyr Lys Thr Val Lys Gly Ser Arg Val Glu Trp Leu Val Asn Lys Val
 1155 1160 1165
 Arg Gly Tyr His Val Leu Leu Val Ser Glu Tyr Asn Leu Ala Leu Pro
 1170 1175 1180
 Arg Arg Arg Val Thr Trp Leu Ser Pro Leu Asn Val Thr Gly Ala Asp
 1185 1190 1195 1200
 Arg Cys Tyr Asp Leu Ser Leu Gly Leu Pro Ala Asp Ala Gly Arg Phe
 1205 1210 1215
 Asp Leu Val Phe Val Asn Ile His Thr Glu Phe Arg Ile His His Tyr
 1220 1225 1230
 Gln Gln Cys Val Asp His Ala Met Lys Leu Gln Met Leu Gly Gly Asp
 1235 1240 1245
 Ala Leu Arg Leu Leu Lys Pro Gly Gly Ile Leu Met Arg Ala Tyr Gly
 1250 1255 1260
 Tyr Ala Asp Lys Ile Ser Glu Ala Val Val Ser Ser Leu Ser Arg Lys
 1265 1270 1275 1280
 Phe Ser Ser Ala Arg Val Leu Arg Pro Asp Cys Val Thr Ser Asn Thr
 1285 1290 1295
 Glu Val Phe Leu Leu Phe Ser Asn Phe Asp Asn Gly Lys Arg Pro Ser
 1300 1305 1310
 Thr Leu His Gln Met Asn Thr Lys Leu Ser Ala Val Tyr Ala Gly Glu
 1315 1320 1325
 Ala Met His Thr Ala Gly Cys Ala Pro Ser Tyr Arg Val Lys Arg Ala
 1330 1335 1340
 Asp Ile Ala Thr Cys Thr Glu Ala Ala Val Val Asn Ala Ala Asn Ala
 1345 1350 1355 1360
 Arg Gly Thr Val Gly Asp Gly Val Cys Arg Ala Val Ala Lys Lys Trp
 1365 1370 1375
 Pro Ser Ala Phe Lys Gly Ala Ala Thr Pro Val Gly Thr Ile Lys Thr
 1380 1385 1390
 Val Met Cys Gly Ser Tyr Pro Val Ile His Ala Val Ala Pro Asn Phe

1395

1400

1405

Ser Ala Thr Thr Glu Ala Glu Gly Asp Arg Glu Leu Ala Ala Val Tyr
 1410 1415 1420

Arg Ala Val Ala Ala Glu Val Asn Arg Leu Ser Leu Ser Ser Val Ala
 1425 1430 1435 1440

Ile Pro Leu Leu Ser Thr Gly Val Phe Ser Gly Gly Arg Asp Arg Leu
 1445 1450 1455

Gln Gln Ser Leu Asn His Leu Phe Thr Ala Met Asp Ala Thr Asp Ala
 1460 1465 1470

Asp Val Thr Ile Tyr Cys Arg Asp Lys Ser Trp Glu Lys Lys Ile Gln
 1475 1480 1485

Glu Ala Ile Asp Met Arg Thr Ala Val Glu Leu Leu Asn Asp Asp Val
 1490 1495 1500

Glu Leu Thr Thr Asp Leu Val Arg Val His Pro Asp Ser Ser Leu Val
 1505 1510 1515 1520

Gly Arg Lys Gly Tyr Ser Thr Thr Asp Gly Ser Leu Tyr Ser Tyr Phe
 1525 1530 1535

Glu Gly Thr Lys Phe Asn Gln Ala Ala Ile Asp Met Ala Glu Ile Leu
 1540 1545 1550

Thr Leu Trp Pro Arg Leu Gln Glu Ala Asn Glu Gln Ile Cys Leu Tyr
 1555 1560 1565

Ala Leu Gly Glu Thr Met Asp Asn Ile Arg Ser Lys Cys Pro Val Asn
 1570 1575 1580

Asp Ser Asp Ser Ser Thr Pro Pro Arg Thr Val Pro Cys Leu Cys Arg
 1585 1590 1595 1600

Tyr Ala Met Thr Ala Glu Arg Ile Ala Arg Leu Arg Ser His Gln Val
 1605 1610 1615

Lys Ser Met Val Val Cys Ser Ser Phe Pro Leu Pro Lys Tyr His Val
 1620 1625 1630

Asp Gly Val Gln Lys Val Lys Cys Glu Lys Val Leu Leu Phe Asp Pro
 1635 1640 1645

Thr Val Pro Ser Val Val Ser Pro Arg Lys Tyr Ala Ala Ser Thr Thr
 1650 1655 1660

Asp His Ser Asp Arg Ser Leu Arg Gly Phe Asp Leu Asp Trp Thr Thr
 1665 1670 1675 1680

Asp Ser Ser Ser Thr Ala Ser Asp Thr Met Ser Leu Pro Ser Leu Gln
 1685 1690 1695
 Ser Cys Asp Ile Asp Ser Ile Tyr Glu Pro Met Ala Pro Ile Val Val
 1700 1705 1710
 Thr Ala Asp Val His Pro Glu Pro Ala Gly Ile Ala Asp Leu Ala Ala
 1715 1720 1725
 Asp Val His Pro Glu Pro Ala Asp His Val Asp Leu Glu Asn Pro Ile
 1730 1735 1740
 Pro Pro Pro Arg Pro Lys Arg Ala Ala Tyr Leu Ala Ser Arg Ala Ala
 1745 1750 1755 1760
 Glu Arg Pro Val Pro Ala Pro Arg Lys Pro Thr Pro Ala Pro Arg Thr
 1765 1770 1775
 Ala Phe Arg Asn Lys Leu Pro Leu Thr Phe Gly Asp Phe Asp Glu His
 1780 1785 1790
 Glu Val Asp Ala Leu Ala Ser Gly Ile Thr Phe Gly Asp Phe Asp Asp
 1795 1800 1805
 Val Leu Arg Leu Gly Arg Ala Gly Ala Tyr Ile Phe Ser Ser Asp Thr
 1810 1815 1820
 Gly Ser Gly His Leu Gln Gln Lys Ser Val Arg Gln His Asn Leu Gln
 1825 1830 1835 1840
 Cys Ala Gln Leu Asp Ala Val Gln Glu Glu Lys Met Tyr Pro Pro Lys
 1845 1850 1855
 Leu Asp Thr Glu Arg Glu Lys Leu Leu Leu Leu Lys Met Gln Met His
 1860 1865 1870
 Pro Ser Glu Ala Asn Lys Ser Arg Tyr Gln Ser Arg Lys Val Glu Asn
 1875 1880 1885
 Met Lys Ala Thr Val Val Asp Arg Leu Thr Ser Gly Ala Arg Leu Tyr
 1890 1895 1900
 Thr Gly Ala Asp Val Gly Arg Ile Pro Thr Tyr Ala Val Arg Tyr Pro
 1905 1910 1915 1920
 Arg Pro Val Tyr Ser Pro Thr Val Ile Glu Arg Phe Ser Ser Pro Asp
 1925 1930 1935
 Val Ala Ile Ala Ala Cys Asn Glu Tyr Leu Ser Arg Asn Tyr Pro Thr
 1940 1945 1950

Val Ala Ser Tyr Gln Ile Thr Asp Glu Tyr Asp Ala Tyr Leu Asp Met
 1955 1960 1965
 Val Asp Gly Ser Asp Ser Cys Leu Asp Arg Ala Thr Phe Cys Pro Ala
 1970 1975 1980
 Lys Leu Arg Cys Tyr Pro Lys His His Ala Tyr His Gln Pro Thr Val
 1985 1990 1995 2000
 Arg Ser Ala Val Pro Ser Pro Phe Gln Asn Thr Leu Gln Asn Val Leu
 2005 2010 2015
 Ala Ala Ala Thr Lys Arg Asn Cys Asn Val Thr Gln Met Arg Glu Leu
 2020 2025 2030
 Pro Thr Met Asp Ser Ala Val Phe Asn Val Glu Cys Phe Lys Arg Tyr
 2035 2040 2045
 Ala Cys Ser Gly Glu Tyr Trp Glu Glu Tyr Ala Lys Gln Pro Ile Arg
 2050 2055 2060
 Ile Thr Thr Glu Asn Ile Thr Thr Tyr Val Thr Lys Leu Lys Gly Pro
 2065 2070 2075 2080
 Lys Ala Ala Ala Leu Phe Ala Lys Thr His Asn Leu Val Pro Leu Gln
 2085 2090 2095
 Glu Val Pro Met Asp Arg Phe Thr Val Asp Met Lys Arg Asp Val Lys
 2100 2105 2110
 Val Thr Pro Gly Thr Lys His Thr Glu Glu Arg Pro Lys Val Gln Val
 2115 2120 2125
 Ile Gln Ala Ala Glu Pro Leu Ala Thr Ala Tyr Leu Cys Gly Ile His
 2130 2135 2140
 Arg Glu Leu Val Arg Arg Leu Asn Ala Val Leu Arg Pro Asn Val His
 2145 2150 2155 2160
 Thr Leu Phe Asp Met Ser Ala Glu Asp Phe Asp Ala Ile Ile Ala Ser
 2165 2170 2175
 His Phe His Pro Gly Asp Pro Val Leu Glu Thr Asp Ile Ala Ser Phe
 2180 2185 2190
 Asp Lys Ser Gln Asp Asp Ser Leu Ala Leu Thr Gly Leu Met Ile Leu
 2195 2200 2205
 Glu Asp Leu Gly Val Asp Gln Tyr Leu Leu Asp Leu Ile Glu Ala Ala
 2210 2215 2220

Phe Gly Glu Ile Ser Ser Cys His Leu Pro Thr Gly Thr Arg Phe Lys
 2225 2230 2235 2240
 Phe Gly Ala Met Met Lys Ser Gly Met Phe Leu Thr Leu Phe Ile Asn
 2245 2250 2255
 Thr Val Leu Asn Ile Thr Ile Ala Ser Arg Val Leu Glu Gln Arg Leu
 2260 2265 2270
 Thr Asp Ser Ala Cys Ala Ala Phe Ile Gly Asp Asp Asn Ile Val His
 2275 2280 2285
 Gly Val Ile Ser Asp Lys Leu Met Ala Glu Arg Cys Ala Ser Trp Val
 2290 2295 2300
 Asn Met Glu Val Lys Ile Ile Asp Ala Val Met Gly Glu Lys Pro Pro
 2305 2310 2315 2320
 Tyr Phe Cys Gly Gly Phe Ile Val Phe Asp Ser Val Thr Gln Thr Ala
 2325 2330 2335
 Cys Arg Val Ser Asp Pro Leu Lys Arg Leu Phe Lys Leu Gly Lys Pro
 2340 2345 2350
 Leu Thr Ala Glu Asp Lys Gln Asp Glu Asp Arg Arg Arg Ala Leu Ser
 2355 2360 2365
 Asp Glu Val Ser Lys Trp Phe Arg Thr Gly Leu Gly Ala Glu Leu Glu
 2370 2375 2380
 Val Ala Leu Thr Ser Arg Tyr Glu Val Glu Gly Cys Lys Ser Ile Leu
 2385 2390 2395 2400
 Ile Ala Met Thr Thr Leu Ala Arg Asp Ile Lys Ala Phe Lys Lys Leu
 2405 2410 2415
 Arg Gly Pro Val Ile His Leu Tyr Gly Gly Pro Arg Leu Val Arg
 2420 2425 2430

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1253 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Asn Tyr Ile Pro Thr Gln Thr Phe Tyr Gly Arg Arg Trp Arg Pro
 1 5 10 15
 Arg Pro Ala Ala Arg Pro Trp Pro Leu Gln Ala Thr Pro Val Ala Pro
 20 25 30
 Val Val Pro Asp Phe Gln Ala Gln Gln Met Gln Gln Leu Ile Ser Ala
 35 40 45
 Val Asn Ala Leu Thr Met Arg Gln Asn Ala Ile Ala Pro Ala Arg Pro
 50 55 60
 Pro Lys Pro Lys Lys Lys Lys Thr Thr Lys Pro Lys Pro Lys Thr Gln
 65 70 75 80
 Pro Lys Lys Ile Asn Gly Lys Thr Gln Gln Gln Lys Lys Lys Asp Lys
 85 90 95
 Gln Ala Asp Lys Lys Lys Lys Lys Pro Gly Lys Arg Glu Arg Met Cys
 100 105 110
 Met Lys Ile Glu Asn Asp Cys Ile Phe Glu Val Lys His Glu Gly Lys
 115 120 125
 Val Thr Gly Tyr Ala Cys Leu Val Gly Asp Lys Val Met Lys Pro Ala
 130 135 140
 His Val Lys Gly Val Ile Asp Asn Ala Asp Leu Ala Lys Leu Ala Phe
 145 150 155 160
 Lys Lys Ser Ser Lys Tyr Asp Leu Glu Cys Ala Gln Ile Pro Val His
 165 170 175
 Met Arg Ser Asp Ala Ser Lys Tyr Thr His Glu Lys Pro Glu Gly His
 180 185 190
 Tyr Asn Trp His His Gly Ala Val Gln Tyr Ser Gly Gly Arg Phe Thr
 195 200 205
 Ile Pro Thr Gly Ala Gly Lys Pro Gly Asp Ser Gly Arg Pro Ile Phe
 210 215 220
 Asp Asn Lys Gly Arg Val Val Ala Ile Val Leu Gly Gly Ala Asn Glu
 225 230 235 240
 Gly Ser Arg Thr Ala Leu Ser Val Val Thr Trp Asn Lys Asp Met Val
 245 250 255
 Thr Arg Val Thr Pro Glu Gly Ser Glu Glu Trp Ser Ala Pro Leu Ile
 260 265 270

Thr Ala Met Cys Val Leu Ala Asn Ala Thr Phe Pro Cys Phe Gln Pro
 275 280 285
 Pro Cys Val Pro Cys Cys Tyr Glu Asn Asn Ala Glu Ala Thr Leu Arg
 290 295 300
 Met Leu Glu Asp Asn Val Asp Arg Pro Gly Tyr Tyr Asp Leu Leu Gln
 305 310 315 320
 Ala Ala Leu Thr Cys Arg Asn Gly Thr Arg His Arg Arg Ser Val Ser
 325 330 335
 Gln His Phe Asn Val Tyr Lys Ala Thr Arg Pro Tyr Ile Ala Tyr Cys
 340 345 350
 Ala Asp Cys Gly Ala Gly His Ser Cys His Ser Pro Val Ala Ile Glu
 355 360 365
 Ala Val Arg Ser Glu Ala Thr Asp Gly Met Leu Lys Ile Gln Phe Ser
 370 375 380
 Ala Gln Ile Gly Ile Asp Lys Ser Asp Asn His Asp Tyr Thr Lys Ile
 385 390 395 400
 Arg Tyr Ala Asp Gly His Ala Ile Glu Asn Ala Val Arg Ser Ser Leu
 405 410 415
 Lys Val Ala Thr Ser Gly Asp Cys Phe Val His Gly Thr Met Gly His
 420 425 430
 Phe Ile Leu Ala Lys Cys Pro Pro Gly Glu Phe Leu Gln Val Ser Ile
 435 440 445
 Gln Asp Thr Arg Asn Ala Val Arg Ala Cys Arg Ile Gln Tyr His His
 450 455 460
 Asp Pro Gln Pro Val Gly Arg Glu Lys Phe Thr Ile Arg Pro His Tyr
 465 470 475 480
 Gly Lys Glu Ile Pro Cys Thr Thr Tyr Gln Gln Thr Thr Ala Lys Thr
 485 490 495
 Val Glu Glu Ile Asp Met His Met Pro Pro Asp Thr Pro Asp Arg Thr
 500 505 510
 Leu Leu Ser Gln Gln Ser Gly Asn Val Lys Ile Thr Val Gly Gly Lys
 515 520 525
 Lys Val Lys Tyr Asn Cys Thr Cys Gly Thr Gly Asn Val Gly Thr Thr
 530 535 540

Asn	Ser	Asp	Met	Thr	Ile	Asn	Thr	Cys	Leu	Ile	Glu	Gln	Cys	His	Val
545					550					555					560
Ser	Val	Thr	Asp	His	Lys	Lys	Trp	Gln	Phe	Asn	Ser	Pro	Phe	Val	Pro
				565					570					575	
Arg	Ala	Asp	Glu	Pro	Ala	Arg	Lys	Gly	Lys	Val	His	Ile	Pro	Phe	Pro
			580					585					590		
Leu	Asp	Asn	Ile	Thr	Cys	Arg	Val	Pro	Met	Ala	Arg	Glu	Pro	Thr	Val
		595					600					605			
Ile	His	Gly	Lys	Arg	Glu	Val	Thr	Leu	His	Leu	His	Pro	Asp	His	Pro
	610					615					620				
Thr	Leu	Phe	Ser	Tyr	Arg	Thr	Leu	Gly	Glu	Asp	Pro	Gln	Tyr	His	Glu
625					630					635					640
Glu	Trp	Val	Thr	Ala	Ala	Val	Glu	Arg	Thr	Ile	Pro	Val	Pro	Val	Asp
				645					650					655	
Gly	Met	Glu	Tyr	His	Trp	Gly	Asn	Asn	Asp	Pro	Val	Arg	Leu	Trp	Ser
			660					665					670		
Gln	Leu	Thr	Thr	Glu	Gly	Lys	Pro	His	Gly	Trp	Pro	His	Gln	Ile	Val
		675					680					685			
Gln	Tyr	Tyr	Tyr	Gly	Leu	Tyr	Pro	Ala	Ala	Thr	Val	Ser	Ala	Val	Val
	690					695					700				
Gly	Met	Ser	Leu	Leu	Ala	Leu	Ile	Ser	Ile	Phe	Ala	Ser	Cys	Tyr	Met
705					710					715					720
Leu	Val	Ala	Ala	Arg	Ser	Lys	Cys	Leu	Thr	Pro	Tyr	Ala	Leu	Thr	Pro
				725					730					735	
Gly	Ala	Ala	Val	Pro	Trp	Thr	Leu	Gly	Ile	Leu	Cys	Cys	Ala	Pro	Arg
			740					745					750		
Ala	His	Ala	Ala	Ser	Val	Ala	Glu	Thr	Met	Ala	Tyr	Leu	Trp	Asp	Gln
		755					760					765			
Asn	Gln	Ala	Leu	Phe	Trp	Leu	Glu	Phe	Ala	Ala	Pro	Val	Ala	Cys	Ile
	770					775					780				
Leu	Ile	Ile	Thr	Tyr	Cys	Leu	Arg	Asn	Val	Leu	Cys	Cys	Cys	Lys	Ser
785					790					795					800
Leu	Ser	Phe	Leu	Val	Leu	Leu	Ser	Leu	Gly	Ala	Thr	Ala	Arg	Ala	Tyr
			805						810					815	

Glu His Ser Thr Val Met Pro Asn Val Val Gly Phe Pro Tyr Lys Ala
 820 825 830
 His Ile Glu Arg Pro Gly Tyr Ser Pro Leu Thr Leu Gln Met Gln Val
 835 840 845
 Val Glu Thr Ser Leu Glu Pro Thr Leu Asn Leu Glu Tyr Ile Thr Cys
 850 855 860
 Glu Tyr Lys Thr Val Val Pro Ser Pro Tyr Val Lys Cys Cys Gly Ala
 865 870 875 880
 Ser Glu Cys Ser Thr Lys Glu Lys Pro Asp Tyr Gln Cys Lys Val Tyr
 885 890 895
 Thr Gly Val Tyr Pro Phe Met Trp Gly Gly Ala Tyr Cys Phe Cys Asp
 900 905 910
 Ser Glu Asn Thr Gln Leu Ser Glu Ala Tyr Val Asp Arg Ser Asp Val
 915 920 925
 Cys Arg His Asp His Ala Ser Ala Tyr Lys Ala His Thr Ala Ser Leu
 930 935 940
 Lys Ala Lys Val Arg Val Met Tyr Gly Asn Val Asn Gln Thr Val Asp
 945 950 955 960
 Val Tyr Val Asn Gly Asp His Ala Val Thr Ile Gly Gly Thr Gln Phe
 965 970 975
 Ile Phe Gly Pro Leu Ser Ser Ala Trp Thr Pro Phe Asp Asn Lys Ile
 980 985 990
 Val Val Tyr Lys Asp Glu Val Phe Asn Gln Asp Phe Pro Pro Tyr Gly
 995 1000 1005
 Ser Gly Gln Pro Gly Arg Phe Gly Asp Ile Gln Ser Arg Thr Val Glu
 1010 1015 1020
 Ser Asn Asp Leu Tyr Ala Asn Thr Ala Leu Lys Leu Ala Arg Pro Ser
 1025 1030 1035 1040
 Pro Gly Met Val His Val Pro Tyr Thr Gln Thr Pro Ser Gly Phe Lys
 1045 1050 1055
 Tyr Trp Leu Lys Glu Lys Gly Thr Ala Leu Asn Thr Lys Ala Pro Phe
 1060 1065 1070
 Gly Cys Gln Ile Lys Thr Asn Pro Val Arg Ala Met Asn Cys Ala Val
 1075 1080 1085

Gly Asn Ile Pro Val Ser Met Asn Leu Pro Asp Ser Ala Phe Thr Arg
 1090 1095 1100
 Ile Val Glu Ala Pro Thr Ile Ile Asp Leu Thr Cys Thr Val Ala Thr
 1105 1110 1115 1120
 Cys Thr His Ser Ser Asp Phe Gly Gly Val Leu Thr Leu Thr Tyr Lys
 1125 1130 1135
 Thr Asn Lys Asn Gly Asp Cys Ser Val His Ser His Ser Asn Val Ala
 1140 1145 1150
 Thr Leu Gln Glu Ala Thr Ala Lys Val Lys Thr Ala Gly Lys Val Thr
 1155 1160 1165
 Leu His Phe Ser Thr Ala Ser Ala Ser Pro Ser Phe Val Val Ser Leu
 1170 1175 1180
 Cys Ser Ala Arg Ala Thr Cys Ser Ala Ser Cys Glu Pro Pro Lys Asp
 1185 1190 1195 1200
 His Ile Val Pro Tyr Ala Ala Ser His Ser Asn Val Val Phe Pro Asp
 1205 1210 1215
 Met Ser Gly Thr Ala Leu Ser Trp Val Gln Lys Ile Ser Gly Gly Leu
 1220 1225 1230
 Gly Ala Phe Ala Ile Gly Ala Ile Leu Val Leu Val Val Val Thr Cys
 1235 1240 1245
 Ile Gly Leu Arg Arg
 1250

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..115
- (D) OTHER INFORMATION: /label= 26S_region
/note= "26S promoter and transcription start and proximal downstream region of pSFV1; Figure 8."

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /product= "26S promoter region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ACCTCTACGG CGGTCCTAGA TTGGTGCGTT AATACACAGA ATCTGATTGG ATCCCGGGTA 60
 ATTAATTGAA TTACATCCCT ACGCAAACGT TTTACGGCCG CCGGTGGCGC CCGCG 115

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..127
- (D) OTHER INFORMATION: /label= 26S_region
/note= "26S promoter and transcription start and proximal downstream region of pSFV2; Figure 8."

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /product= "26S promoter region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACCTCTACGG CGGTCCTAGA TTGGTGCGTT AATACACAGA ATTCTGATTA TAGCGCACTA 60
 TTATATAGCA CCGGATCCCG GGTAATTAAT TGACGCAAAC GTTTTACGGC CGCCGGTGGC 120

GCCCGCG

127

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..123
- (D) OTHER INFORMATION: /label= 26S_region
/note= "26S promoter and transcription start and proximal downstream region of pSFV3; Figure 8."

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /product= "26S promoter region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ACCTCTACGG CGGTCCTAGA TTGGTGCGTT AATACACAGA ATTCTGATTA TAGCGCACTA 60
 TTATATAGCA CCATGGATCC CGGGTAATTA ATTGACGTTT TACGGCCGCC GGTGGCGCCC 120
 GCG 123

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Semliki Forest Virus

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..54
- (D) OTHER INFORMATION: /label= restrict_site
/note= "sequence of SFV E2 genome in vicinity of Bam HI site
in SFV vector E2; Figure 12."

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..54

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAC	TCA	CCT	TTC	GTC	CCG	AGA	GCC	GAC	GAA	CCG	GCT	AGA	AAA	GGC	AAA	48
Asn	Ser	Pro	Phe	Val	Pro	Arg	Ala	Asp	Glu	Pro	Ala	Arg	Lys	Gly	Lys	
1				5				10						15		

GTC	CAT															54
Val	His															

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asn	Ser	Pro	Phe	Val	Pro	Arg	Ala	Asp	Glu	Pro	Ala	Arg	Lys	Gly	Lys
1				5				10						15	
Val	His														

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: HIV

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..46

(D) OTHER INFORMATION: /label= fragment

/note= "HIV gp120 epitope introduced into SFV
vector E2; Figure 12."

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAT	CCG	CGT	ATC	CAG	AGA	GGA	CCA	GGA	AGA	GCA	TTT	GTT	GAG	CTA	
Asp	Pro	Arg	Ile	Gln	Arg	Gly	Pro	Gly	Arg	Ala	Phe	Val	Glu	Leu	
1				5				10					15		

45

46

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Asp	Pro	Arg	Ile	Gln	Arg	Gly	Pro	Gly	Arg	Ala	Phe	Val	Glu	Leu	
1				5				10					15		

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..51
- (D) OTHER INFORMATION: /label= chimaeric_seq
/note= "SFV-HIV chimaeric sequence shown in Figure 12."

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..51
- (D) OTHER INFORMATION: /product= "SFV-HIV chimaeric sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAG	GAT	CCG	CGT	ATC	CAG	AGA	GGA	CCA	GGA	AGA	GCA	TTT	GTT	GAG	GAT	48
Glu	Asp	Pro	Arg	Ile	Gln	Arg	Gly	Pro	Gly	Arg	Ala	Phe	Val	Glu	Asp	
1				5				10						15		

CCG																51
Pro																

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Glu	Asp	Pro	Arg	Ile	Gln	Arg	Gly	Pro	Gly	Arg	Ala	Phe	Val	Glu	Asp
1				5				10						15	

Pro

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..60

(D) OTHER INFORMATION: /label= oligonucleotide
/note= "used to introduce new linker site"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGGCCAGTGA ATTCTGATTG GATCCCGGGT AATTAATTGA ATTACATCCC TACGCAAACG

60

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..62

(D) OTHER INFORMATION: /label= oligonucleotide
/note= "used to introduce new linker site"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCGCACTATT ATAGCACCGG CTCCCGGGTA ATTAATTGAC GCAAACGTTT TACGGCCGCC

60

GG

62

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..62

(D) OTHER INFORMATION: /label= oligonucleotide
/note= "used to introduce new linker site"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCGCACTATT ATAGCACCAT GGATCCGGGT AATTAATTGA CGTTTTACGG CCGCCGGTGG 60

CG 62

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..21

(D) OTHER INFORMATION: /label= primer
/note= "SP1 upstream sequencing primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGGCGGTCCT AGATTGGTGC G 21

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..21

(D) OTHER INFORMATION: /label= primer

/note= "SP2 downstream sequencing primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGCGGGCGCC ACCGGCGGCC G

21

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..21

(D) OTHER INFORMATION: /label= primer

/note= "primer-1 for first strand cDNA synthesis"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTTCTCGTAG TTCTCCTCGT C

21

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..27

(D) OTHER INFORMATION: /label= primer

/note= "primer-2 for first strand cDNA synthesis"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GTATCCCGAG TGGTTGTTCT CGTAATA

27

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..28

(D) OTHER INFORMATION: /label= primer

/note= "5' most primer for second strand cDNA
synthesis, equals bp 1-28 of SFV sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATGGCGGATG TGTGACATAC ACGACGCC

28

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..46
- (D) OTHER INFORMATION: /label= adaptor
/note= "5'-sticky end
(EcoRI-HindIII-NotI-XmaIII-SpeI) blunt end-3'
adaptor"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AAATTCAAGCT TCGGCCCGCA CTAGTGTTCG AACGCCGGCG TGATCA

46

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..8
- (D) OTHER INFORMATION: /label= oligonucleotide
/note= "NcoI oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GCCATGGC

8

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /label= oligonucleotide
/note= "oligonucleotide used for screening by
colony hybridization"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGTGACACTA TAGCCATGGC

20

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /label= oligonucleotide
/note= "site-directed mutagenic oligonucleotide
used to introduce a BamHI site into the SFV
genome"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GATCGGCCTA GGAGCCGAGA GCCC

24

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Semliki Forest Virus

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..80
- (D) OTHER INFORMATION: /label= terminator
/note= "3' terminal sequence of cDNA expression
vector complementary to alphavirus genomic RNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TTTCCAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 60
 AAAAAAAAAA AAAAAGTAGT 80

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Semliki Forest Virus

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..54
- (D) OTHER INFORMATION: /label= restrict_site
/note= "sequence of SFV vector E2 in vicinity of Bam HI site;
Figure 12."

(ix) FEATURE:

- (A) NAME/KEY: mutation
- (B) LOCATION: 27..32
- (D) OTHER INFORMATION: /label= restriction_sit
/note= "BamHI recognition sequence introduced into
SFV E2 genome in SFV vector E2."

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..54

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AAC TCA CCT TTC GTC CCG AGA GCC GAG GAT CCG GCT AGA AAA GGC AAA 48
Asn Ser Pro Phe Val Pro Arg Ala Glu Asp Pro Ala Arg Lys Gly Lys
1 5 10 15
GTC CAT 54
Val His

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Asn Ser Pro Phe Val Pro Arg Ala Glu Asp Pro Ala Arg Lys Gly Lys
1 5 10 15
Val His